


```

ORIGIN
Query Match          74.4%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactcctggaagc 16
    ||||| ||||| |||
Db 3 ATCACTCCTGGCAGC 17

RESULT 2
AX217700
LOCUS          AX217700          17 bp mRNA linear PAT 07-SEP-2001
DEFINITION    Sequence 3142 from Patent WO0159103.
ACCESSION     AX217700
VERSION       AX217700.1 GI:15527761
KEYWORDS      .
SOURCE        synthetic construct.
ORGANISM      synthetic construct
              artificial sequence.
REFERENCE     1 (bases 1 to 17)
AUTHORS      Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE        Method and reagent for the modulation and diagnosis of cd20 and
              nogo gene expression
JOURNAL       Patent: WO 0159103-A 3142 16-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
              McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES      .
              Location/Qualifiers
              source
              1..17
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Nucleic Acid"
              4 a 6 c 4 g 3 t
BASE COUNT    4 a 6 c 4 g 3 t
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Query Match          74.4%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactcctggaagc 16
    ||||| ||||| |||
Db 3 ATCACTCCTGGCAGC 17

RESULT 2
AX217700
LOCUS          AX217700          17 bp mRNA linear PAT 07-SEP-2001
DEFINITION    Sequence 3142 from Patent WO0159103.
ACCESSION     AX217700
VERSION       AX217700.1 GI:15527761
KEYWORDS      .
SOURCE        synthetic construct.
ORGANISM      synthetic construct
              artificial sequence.
REFERENCE     1 (bases 1 to 17)
AUTHORS      Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE        Method and reagent for the modulation and diagnosis of cd20 and
              nogo gene expression
JOURNAL       Patent: WO 0159103-A 3143 16-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
              McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES      .
              Location/Qualifiers
              source
              1..17
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Nucleic Acid"
              5 a 6 c 3 g 3 t
BASE COUNT    5 a 6 c 3 g 3 t
ORIGIN

ORIGIN
Query Match          74.4%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactcctggaagc 16
    ||||| ||||| |||
Db 1 ATCACTCCTGGCAGC 15

RESULT 4
AR084474/c
LOCUS          AR084474          31 bp DNA linear PAT 01-SEP-2000
DEFINITION    Sequence 10 from patent US 5981183.
ACCESSION     AR084474
VERSION       AR084474.1 GI:10011245
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
              Unclassified.
REFERENCE     1 (bases 1 to 31)
AUTHORS      Takarada,Y., Inoue,H., Shibata,S. and Kawamura,Y.
TITLE        Method for amplifying and detecting of target nucleic acid sequence
              using thermostable enzyme
JOURNAL       Patent: US 5981183-A 10 09-NOV-1999;
              Location/Qualifiers
              source
              1..31
              /organism="unknown"
              5 a 9 c 8 g 9 t
BASE COUNT    5 a 9 c 8 g 9 t
ORIGIN

Query Match          73.3%; Score 13.2; DB 6; Length 31;
Best Local Similarity 83.3%; Pred. No. 7.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcactcctggaagccc 18
    || ||||| ||||| |||||
Db 27 TAGCACCCATGGAAGCCC 10

RESULT 5
AR172373/c
LOCUS          AR172373          31 bp DNA linear PAT 17-DEC-2001
DEFINITION    Sequence 10 from patent US 6303306.
ACCESSION     AR172373
VERSION       AR172373.1 GI:17911864
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
              Unclassified.
REFERENCE     1 (bases 1 to 31)
AUTHORS      Takarada,Y., Inoue,H., Shibata,S. and Kawamura,Y.
TITLE        Method for amplifying and detecting of target nucleic acid sequence
              using thermostable enzyme
JOURNAL       Patent: US 6303306-A 10 16-OCT-2001;
              Location/Qualifiers
              source
              1..31
              /organism="unknown"
              5 a 9 c 8 g 9 t
BASE COUNT    5 a 9 c 8 g 9 t
ORIGIN

Query Match          73.3%; Score 13.2; DB 6; Length 31;
Best Local Similarity 83.3%; Pred. No. 7.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcactcctggaagccc 18
    || ||||| ||||| |||||
Db 27 TAGCACCCATGGAAGCCC 10

RESULT 6
AR126586

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LOCUS       AR126586                      20 bp    DNA
DEFINITION   Sequence 15 from patent US 6180353.
ACCESSION    AR126586
VERSION      AR126586.1  GI:14113179
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Dean,N.M. and Cowsert,L.M.
TITLE       Antisense modulation of daxx expression
JOURNAL     Patent: US 6180353-A 15 30-JAN-2001;
            Location/Qualifiers
FEATURES             source
BASE COUNT   2 a 6 c 7 g 5 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcactcctggaagc 16
Db 4 TCTCGCTCCTGGAAGC 19

RESULT 7
LOCUS       AR129611                      20 bp    DNA
DEFINITION   Sequence 15 from patent US 6187545.
ACCESSION    AR129611
VERSION      AR129611.1  GI:14117508
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     McKay,R., Butler,M.M., Wyatt,J. and Cowsert,L.M.
TITLE       Antisense modulation of pepck-cytosolic expression
JOURNAL     Patent: US 6187545-A 15 13-FEB-2001;
            Location/Qualifiers
FEATURES             source
BASE COUNT   2 a 6 c 7 g 5 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcactcctggaagc 16
Db 4 TCTCGCTCCTGGAAGC 19

RESULT 8
LOCUS       AR162335                      20 bp    DNA
DEFINITION   Sequence 15 from patent US 6258600.
ACCESSION    AR162335
VERSION      AR162335.1  GI:16229500
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Zhang,H. and Cowsert,L.M.
TITLE       Antisense modulation of caspase 8 expression
JOURNAL     Patent: US 6258600-A 15 10-JUL-2001;
            Location/Qualifiers
FEATURES             source
BASE COUNT   2 a 6 c 7 g 5 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcactcctggaagc 16
Db 4 TCTCGCTCCTGGAAGC 19

LOCUS       AR126586                      20 bp    DNA
DEFINITION   Sequence 15 from patent US 6180353.
ACCESSION    AR126586
VERSION      AR126586.1  GI:14113179
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Dean,N.M. and Cowsert,L.M.
TITLE       Antisense modulation of daxx expression
JOURNAL     Patent: US 6180353-A 15 30-JAN-2001;
            Location/Qualifiers
FEATURES             source
BASE COUNT   2 a 6 c 7 g 5 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcactcctggaagc 16
Db 4 TCTCGCTCCTGGAAGC 19

RESULT 9
LOCUS       AR163817                      20 bp    DNA
DEFINITION   Sequence 15 from patent US 6271030.
ACCESSION    AR163817
VERSION      AR163817.1  GI:16234584
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE       Antisense inhibition of C/EBP beta expression
JOURNAL     Patent: US 6271030-A 15 07-AUG-2001;
            Location/Qualifiers
FEATURES             source
BASE COUNT   2 a 6 c 7 g 5 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcactcctggaagc 16
Db 4 TCTCGCTCCTGGAAGC 19

RESULT 10
LOCUS       AR172890                      20 bp    DNA
DEFINITION   Sequence 15 from patent US 6303374.
ACCESSION    AR172890
VERSION      AR172890.1  GI:17912381
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Zhang,H. and Cowsert,L.M.
TITLE       Antisense modulation of caspase 3 expression
JOURNAL     Patent: US 6303374-A 15 16-OCT-2001;
            Location/Qualifiers
FEATURES             source
BASE COUNT   2 a 6 c 7 g 5 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcactcctggaagc 16
Db 4 TCTCGCTCCTGGAAGC 19

LOCUS       AR163817                      20 bp    DNA
DEFINITION   Sequence 15 from patent US 6271030.
ACCESSION    AR163817
VERSION      AR163817.1  GI:16234584
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE       Antisense inhibition of C/EBP beta expression
JOURNAL     Patent: US 6271030-A 15 07-AUG-2001;
            Location/Qualifiers
FEATURES             source
BASE COUNT   2 a 6 c 7 g 5 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcactcctggaagc 16
Db 4 TCTCGCTCCTGGAAGC 19

RESULT 11
LOCUS       AR172890                      20 bp    DNA
DEFINITION   Sequence 15 from patent US 6303374.
ACCESSION    AR172890
VERSION      AR172890.1  GI:17912381
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Zhang,H. and Cowsert,L.M.
TITLE       Antisense modulation of caspase 3 expression
JOURNAL     Patent: US 6303374-A 15 16-OCT-2001;
            Location/Qualifiers
FEATURES             source
BASE COUNT   2 a 6 c 7 g 5 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcactcctggaagc 16
Db 4 TCTCGCTCCTGGAAGC 19
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RESULT 11
LOCUS ARI73817 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 15 from patent US 6306606.
ACCESSION ARI73817
VERSION ARI73817.1 GI:17914137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weber,M.J., Wyatt,J. and Cowser,L.M.
TITLE Antisense modulation of MP-1 expression
JOURNAL Patent: US 6306606-A 15 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 2 a 6 c 7 g 5 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 TCTCGCTCTCTGGAAGC 19

RESULT 12
LOCUS ARI74355 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 15 from patent US 6306655.
ACCESSION ARI74355
VERSION ARI74355.1 GI:17914675
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP alpha expression
JOURNAL Patent: US 6306655-A 15 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 2 a 6 c 7 g 5 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 TCTCGCTCTCTGGAAGC 19

RESULT 13
LOCUS AR089898/c 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 18 from patent US 5994076.
ACCESSION AR089898
VERSION AR089898.1 GI:10016653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
/organism="unknown"

AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 18 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..26
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BASE COUNT 4 a 5 c 8 g 9 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 26;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcactctctggaagc 16
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Db 22 TATGACACCTCTGGAAGC 7

RESULT 14
LOCUS AX249458/c 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1537 from Patent WO0166800.
ACCESSION AX249458
VERSION AX249458.1 GI:15864081
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 31)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1537 13-SEP-2001;
FEATURES Location/Qualifiers
source 1..31
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/db_xref="taxon:9606"
BASE COUNT 10 a 6 c 7 g 7 t 1 others
ORIGIN

Query Match 70.0%; Score 12.6; DB 6; Length 31;
Best Local Similarity 92.3%; Pred. No. 1.7e+04;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tcactctctggaag 15
| | | | | | | | | | | | | | | |
Db 25 TCACCTCTCTGGAAG 13

RESULT 15
LOCUS AX217699 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 3141 from Patent WO0159103.
ACCESSION AX217699
VERSION AX217699.1 GI:15527760
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 3141 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 3 a 6 c 5 g 3 t
ORIGIN

/note="Nucleic Acid"

Query Match 68.9%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. NO. 2.2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 atcactcctggaag 15
 | | | | | | | | | |
Db 4 ATCACTCCTGCGAG 17

Search completed: October 12, 2002, 16:51:10
Job time: 8885 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 14:25:35 ; Search time 792.17 Seconds
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Title: US-09-945-131-1
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Sequence: 1 tatcactcttggaagccc 18

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	21	AAAL3829	Murine PDGFR-beta
2	13.8	76.7	50	22	AAL28262	Human SNP oligonuc
3	13.4	74.4	17	23	ABK02766	Human CD20 Hammerh
4	13.4	74.4	17	23	ABK03142	Human CD20 Inozyme
5	13.4	74.4	17	23	ABK03143	Human CD20 Inozyme
c	6	13.4	74.4	50	AAI33976	Human SNP oligonuc
c	7	13.2	73.3	31	AAQ92585	Thermus thermophil
c	8	13.2	73.3	31	AAQ92602	Thermus thermophil
9	13	72.2	28	21	AAZ88272	Granulocyte macrop

10	13	72.2	29	13	AAQ30835	Type III procollag	
11	13	72.2	29	20	AAV83186	Primer for amplif	
c	12	72.2	31	22	AAI31049	Human single nucle	
13	12.8	71.1	20	22	AAS45602	Mouse GAPDH RT-PCR	
14	12.8	71.1	20	22	AAS21535	Mouse GAPDH revers	
15	12.8	71.1	20	22	AAS10515	Mouse GAPDH revers	
16	12.8	71.1	20	22	AAH47971	Mouse GAPDH PCR pr	
17	12.8	71.1	20	22	AAI12329	Mouse GAPDH DNA am	
18	12.8	71.1	20	22	AAF62859	Mouse GAPDH revers	
19	12.8	71.1	20	22	AAF72914	Mouse GAPDH PCR re	
20	12.8	71.1	20	24	ABA02203	Mouse GAPDH quanti	
21	12.8	71.1	20	24	ABA83456	Mouse GAPDH PCR pr	
22	12.8	71.1	23	15	AAQ73528	Alpha-adducin cDNA	
23	12.8	71.1	33	24	ABA96569	Human tyrosinase 9	
c	24	12.8	71.1	41	AAH46672	Human NADH dehydro	
c	25	12.8	71.1	42	AAH46670	Human NADH dehydro	
c	26	12.8	71.1	50	AAI33581	Human SNP oligonuc	
27	12.4	68.9	17	18	AAAX62339	Granule bound star	
28	12.4	68.9	17	23	ABK03141	Human CD20 Inozyme	
29	12.4	68.9	17	23	ABK03702	Human CD20 Amberzy	
30	12.4	68.9	18	17	AAT36945	OVCAL gene exon 11	
31	12.4	68.9	20	21	AAAG3828	Primer DAGKIAAfor	
c	32	12.4	68.9	31	AAAG62577	Granule bound star	
c	33	12.4	68.9	31	AAI30896	Human single nucle	
c	34	12.4	68.9	45	AAAT86960	DNA for soluble I-	
c	35	12.4	68.9	45	AAAT86952	DNA for soluble I-	
36	12.4	68.9	47	21	AAZ69291	Human map-related	
c	37	12.2	67.8	17	AAQ71843	Primer (RB-19) to	
c	38	12.2	67.8	20	AAQ79534	Rat p38alpha antis	
c	39	12.2	67.8	25	AAAC63818	Rhodobacter sphaer	
c	40	12.2	67.8	25	AAZ51058	PCR primer-4 to am	
c	41	12.2	67.8	25	AAZ46832	R. sphaeroides hyd	
c	42	12.2	67.8	30	AAQ27061	HCV primer P32. S	
c	43	12.2	67.8	46	15	AAQ69330	Human mast cell ch
c	44	12.2	67.8	46	18	AAAT63792	Human mast cell ch
c	45	12.2	67.8	46	20	AAAX17080	Test sequence from

ALIGNMENTS

RESULT	1
AAAL3829	
ID	AAAL3829 standard; DNA; 18 BP.
XX	
AC	AAAL3829;
XX	
DF	27-JUL-2000 (first entry)
DE	Murine PDGFR-beta phosphorothioate antisense oligonucleotide SEQ ID NO:1.
DE	
KW	Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW	PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW	recurrent stenosis; cardiovascular injury; ss.
XX	
OS	Mus sp.
XX	
XX	
Key	Location/Qualifiers
FT	modified_base 1..18
FT	/*tag= a
FT	/note= "phosphorothioate linkages"
XX	
PN	CA2228977-A1.
XX	
PD	07-MAY-1999.
XX	
PF	03-FEB-1998; 98CA-2228977.
XX	
PR	07-NOV-1997; 97CA-2215360.
XX	
XX	(EDEL/) EDELMAN E R.
PA	(ROSE/) ROSENBERG R D.
PA	(SIRO/) SIROIS M G.

PA (SIMO/) SIMONS M.
 XX Edelman ER, Rosenberg RD, Sirolis MG, Simons M;
 XX WPI; 2000-283933/25.
 XX
 PT Antisense inhibition of platelet derived growth factor beta-receptor
 subunit expression for the prevention of restenosis -
 XX
 XX Claim 25; Page 15; 43pp; English.
 XX
 CC A method has been developed for preventing restenosis following vascular
 CC injury by antisense inhibition of platelet derived growth factor
 CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
 CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
 CC canal), especially of a valve in the heart, after surgical correction of
 CC the primary condition) following cardiovascular injury. The present
 CC sequence represents a phosphorothioate antisense oligonucleotide for
 CC murine PDGFR-beta.
 XX
 SQ Sequence 18 BP; 4 A; 7 C; 3 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. NO. 7.2;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taccactctggaagccc 18
 |||||
 Db 1 taccactctggaagccc 18

RESULT 2
 AAL28262
 ID AAL28262 standard; DNA; 50 BP.
 AC AAL28262;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #1470.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesis; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 XX 28-DEC-2000; 2000WO-US35498.
 XX
 XX 28-DEC-1999; 99US-0173419.
 XX
 XX 27-DEC-2000; 2000US-0173419.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Shimkets RA, Leach M;
 XX
 XX WPI; 2001-465210/50.
 XX
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1; Page 1801; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesis, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 XX
 SQ Sequence 50 BP; 9 A; 19 C; 13 G; 9 T; 0 other;

Query Match 76.7%; Score 13.8; DB 22; Length 50;
 Best Local Similarity 88.2%; Pred. NO. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcactctggaagccc 18
 ||| |||||
 Db 12 atcgcctctggaagtc 28
 ||| |||||

RESULT 3
 ABK02766
 ID ABK02766 standard; RNA; 17 BP.
 XX
 AC ABK02766;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 Hammerhead ribozyme #65.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 XX
 PN Synthetic.
 XX
 XX WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04273.
 XX
 XX 11-FEB-2000; 2000US-181797P.
 XX
 XX 28-FEB-2000; 2000US-185516P.
 XX
 XX 06-MAR-2000; 2000US-187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J.
 XX (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, McSwiggen J, Chowrira BM;
 XX

DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,

PT and central nervous system injury -

XX

PS Claim 30; Page 141; 200pp; English.

XX

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOMO).

CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN

CC motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme

CC (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used

CC to cleave RNA of CD20 in the presence of a divalent cation that is

CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce

CC CD20 activity of the cell and treat a patient having a condition

CC associated with the level of CD20. The treatment may further comprise the

CC use of one or more therapies. In particular, the CD20 targeting

CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell

CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky

CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),

CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune

CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting

CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a

CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid

CC may be contacted with a cell to reduce NOGO activity of the cell and

CC treat a patient having a condition associated with the level of NOGO. The

CC treatment may further comprise the use of one or more therapies.

CC In particular, the NOGO-targetting nucleic acid may be used to treat

CC central nervous system (CNS) injury and cerebrovascular accident (CVA,

CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The

CC present sequence is a hammerhead ribozyme of the invention.

XX

SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 U; 0 other;

Query Match 74.4%; Score 13.4; DB 23; Length 17;

Best Local Similarity 73.3%; Pred. No. 1.6e+03;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 atcaactcctggagc 16

I:||||:||||

Db 3 auctacuccggcgc 17

RESULT 4

ABK03142

ID ABK03142 standard; RNA; 17 BP.

XX

AC ABK03142;

XX

DT 12-MAR-2002 (first entry)

DE

DE Human CD20 Inozyme #93.

XX

XX Human; ss: antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

Parkinson's disease; ataxia; Huntington's disease;

Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Homo sapiens.

Synthetic.

WO200159103-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US04273.

11-FEB-2000; 2000US-181797P.

28-FEB-2000; 2000US-185516P.

06-MAR-2000; 2000US-187128P.

(RIBO-) RIBOZYME PHARM INC.

(BLAT/) BLATT L.

(MCSW/) MCSWIGGEN J.

(CHOW/) CHOWRIRA B M.

Blatt L, McSwiggen J, Chowrira BM;

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

constructs, which down regulate expression of a CD20 gene or neurite

growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,

and central nervous system injury -

Claim 30; Page 147; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates

expression of a CD20 gene and a nucleic acid molecule which down

regulates expression of a neurite growth inhibitor gene (NOMO).

The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule

possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN

motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme

(cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used

to cleave RNA of CD20 in the presence of a divalent cation that is

preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce

CD20 activity of the cell and treat a patient having a condition

associated with the level of CD20. The treatment may further comprise the

use of one or more therapies. In particular, the CD20 targeting

nucleic acid may be used to treat lymphoma, leukaemia, B-cell

lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky

immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),

immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune

thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting

nucleic acid is used to cleave RNA of the NOGO gene in the presence of a

divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid

may be contacted with a cell to reduce NOGO activity of the cell and

treat a patient having a condition associated with the level of NOGO. The

treatment may further comprise the use of one or more therapies.

In particular, the NOGO-targetting nucleic acid may be used to treat

central nervous system (CNS) injury and cerebrovascular accident (CVA,

stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

disease, muscular dystrophy, and/or other neurodegenerative disease

states which respond to the modulation of NOGO expression. The

present sequence is a hammerhead ribozyme of the invention.

Sequence 17 BP; 4 A; 6 C; 4 G; 3 U; 0 other;

Query Match 74.4%; Score 13.4; DB 23; Length 17;

Best Local Similarity 73.3%; Pred. No. 1.6e+03;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Sequence 17 BP; 4 A; 6 C; 4 G; 3 U; 0 other;

Query Match 74.4%; Score 13.4; DB 23; Length 17;

Best Local Similarity 73.3%; Pred. No. 1.6e+03;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcaactctggaagc 16
 Db 2 auaacuccuggcagc 16
 RESULT 5
 ID ABK03143
 XX ABK03143 standard; RNA; 17 BP.
 AC ABK03143;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 Inozyme #94.
 XX
 KW Human: ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04273.
 XX
 PR 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 XX
 DR WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 30; Page 147; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN
 CC motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human

CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA),
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is an inozyme of the invention.
 XX
 SQ Sequence 17 BP; 5 A; 6 C; 3 G; 3 U; 0 other;
 Query Match 74.4%; Score 13.4; DB 23; Length 17;
 Best Local Similarity 73.3%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 atcaactctggaagc 16
 Db 1 auaacuccuggcagc 15
 RESULT 6
 AAL33976/c
 ID AAL33976 standard; DNA; 50 BP.
 XX
 AC AAL33976;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #7184.
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1; Page 3448; 4143pp; English.
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,

CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

XX SQ Sequence 50 BP; 13 A; 13 C; 13 G; 11 T; 0 other;

Query Match 74.4%; Score 13.4; DB 22; Length 50;
 Best Local Similarity 93.3%; Pred. No. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctggaagc 16
 | |||||
 DB 22 AACACTCTGGAAGC 8

RESULT 7
 AAQ92585/c
 ID AAQ92585 standard; DNA; 31 BP.

XX AC AAQ92585;

XX DT 25-JAN-1996 (first entry)

XX DE Thermus thermophilus RNA polymerase promoter sequence #5 in PCR primer.

XX KW Primer; promoter; PCR; amplification; reverse transcriptase;

XX KW thermostable; polymerase; Vibrio; ribonuclease; ss.

XX OS Synthetic.

XX PN WO9515399-Al.

XX PD 08-JUN-1995.

XX PF 01-DEC-1994; 94WO-JP02025.

XX PR 01-DEC-1993; 93JP-0301823.

XX PA (TOYM) TOYO BOSEKI KK.

XX PI Inoue H, Kawamura Y, Shibata S, Takarada Y;

XX WPI; 1995-215277/28.

XX PT Amplification of poly:nucleotide(s) using thermostable enzymes -
 PT derived from Thermus thermophilus, allows reduction in non-specific
 PT hybridisation and high specificity.

XX PS Disclosure; Page 12; 59pp; Japanese.

XX CC A novel method is presented to amplify a target nucleic acid sequence
 CC which involves binding a mechanism similar to reverse transcriptase PCR
 CC in which a first primer is bound to a target RNA molecule and the first
 CC cDNA strand is synthesised with a thermostable RNA dependent DNA
 CC polymerase, the RNA strand is removed with a thermostable ribonuclease
 CC H, and the DNA strand is converted to a double stranded form by
 CC amplifying with a thermostable DNA polymerase from a second bound primer.
 CC The process differs by producing more copies of the target RNA strand
 CC with a DNA dependent RNA polymerase. The RNA polymerase primes from a
 CC promoter sequence, such as those shown in AAQ92581-Q92615, which is
 CC attached 5' of the target binding sequence of the first primer, e.g.

CC such as primers AAQ92576-80 for targeting the Vibrio TDH gene. The RNA
 CC produced is recycled back to the cDNA conversion step with the RNA
 CC dependent-DNA polymerase.

XX SQ Sequence 31 BP; 5 A; 9 C; 8 G; 9 T; 0 other;

Query Match 73.3%; Score 13.2; DB 16; Length 31;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcactctctggaagccc 18
 || ||| | |||||
 DB 27 TAGCACCCTGGAAGCCC 10

RESULT 8

AAQ92602/c

XX ID AAQ92602 standard; DNA; 31 BP.

XX AC AAQ92602;

XX DT 25-JAN-1996 (first entry)

XX DE Thermus thermophilus RNA polymerase promoter sequence #22 in PCR primer.

XX KW Primer; promoter; PCR; amplification; reverse transcriptase;

XX KW thermostable; polymerase; Vibrio; ribonuclease; ss.

XX OS Synthetic.

XX PN WO9515399-Al.

XX PD 08-JUN-1995.

XX PF 01-DEC-1994; 94WO-JP02025.

XX PR 01-DEC-1993; 93JP-0301823.

XX PA (TOYM) TOYO BOSEKI KK.

XX PI Inoue H, Kawamura Y, Shibata S, Takarada Y;

XX WPI; 1995-215277/28.

XX PT Amplification of poly:nucleotide(s) using thermostable enzymes -
 PT derived from Thermus thermophilus, allows reduction in non-specific
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XX PS Disclosure; Page 13; 59pp; Japanese.

XX CC A novel method is presented to amplify a target nucleic acid sequence
 CC which involves binding a mechanism similar to reverse transcriptase PCR
 CC in which a first primer is bound to a target RNA molecule and the first
 CC cDNA strand is synthesised with a thermostable RNA dependent DNA
 CC polymerase, the RNA strand is removed with a thermostable ribonuclease
 CC H, and the DNA strand is converted to a double stranded form by
 CC amplifying with a thermostable DNA polymerase from a second bound primer.
 CC The process differs by producing more copies of the target RNA strand
 CC with a DNA dependent RNA polymerase. The RNA polymerase primes from a
 CC promoter sequence, such as those shown in AAQ92581-Q92615, which is
 CC attached 5' of the target binding sequence of the first primer, e.g.
 CC such as primers AAQ92576-80 for targeting the Vibrio TDH gene. The RNA
 CC produced is recycled back to the cDNA conversion step with the RNA
 CC dependent-DNA polymerase.

XX SQ Sequence 31 BP; 5 A; 9 C; 8 G; 9 T; 0 other;

Query Match 73.3%; Score 13.2; DB 16; Length 31;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctactctctggaagccc 18
 || || | |||||
 Db 27 TAGCACCCTGGAAGCCC 10

RESULT 9

AAZ88272
 ID AAZ88272 standard; DNA; 28 BP.
 XX
 AC AAZ88272;
 XX
 DT 02-MAY-2000 (first entry)
 XX
 DE Granulocyte macrophage colony stimulating factor PCR primer #2.
 XX
 KW Sec B; granulocyte macrophage colony stimulating factor; GM-CSF;
 KW protein secretion; PCR primer; ss.
 XX

OS Homo sapiens.
 XX

PN CN1236011-A.
 XX

XX 24-NOV-1999.
 PD

XX 15-MAY-1998; 98CN-0110840.
 PF

XX 15-MAY-1998; 98CN-0110840.
 PR

XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
 PA

XX Gan R, Huang P, Qian Y;
 PI

XX WPI; 2000-148268/14.
 DR

XX Method for using molecule mate to promote protein secretion - using
 PT recombinant expression carrier and prokaryote host cell
 PT

XX Example 2; Page 12; 29pp; Chinese.
 PS

XX The present invention uses the co-expression of molecule mate and
 CC required protein in prokaryotic cell, especially colon Bacillus host,
 CC to promote the secretion expression of required protein. Specifically,
 CC the present invention relates to recombinant expression carrier for the
 CC required protein to secret and express in prokaryotic cell and the
 CC expression carrier contains the site after the gene sequence of
 CC encoding molecule mate is connected to the first promoter controllably.
 CC The encoding molecule mate gene sequence has a DNA sequence in the
 CC downstream to connect controllably the encoding required protein gene
 CC sequence to signal peptide containing the second promoter. The present
 CC sequence represents a PCR primer for a human granulocyte macrophage
 CC colony stimulating factor nucleotide sequence which is used in the
 CC exemplification of the present invention.
 XX

SQ Sequence 28 BP; 6 A; 10 C; 5 G; 7 T; 0 other;

Query Match 72.2%; Score 13; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctactctctgga 13
 |||||
 Db 7 tctactctctgga 19

RESULT 10

AAQ30835
 ID AAQ30835 standard; cDNA; 29 BP.
 XX

XX AAQ30835;
 AC

XX 24-MAR-1993 (first entry)
 DT

XX

DE Type III procollagen primer III-2.
 XX

KW Mutation; pro-alpha(III); primer; PCR; ss.
 XX

OS Synthetic.
 XX

PN WO9219754-A.
 XX

PD 12-NOV-1992.
 PD

XX 08-MAY-1992; 92WO-US03866.
 PF

XX 08-MAY-1991; 91US-0696607.
 PR

XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA

XX Kuivaniemi SH, Prockop DJ, Tromp GC;
 PI

XX WPI; 1992-398878/48.
 DR

XX Kit for detecting genetic pre-disposition for vascular aneurysms
 PT - contains primer to amplify portions of Type III procollagen DNA
 PT and detects mutation in standard procollagen DNA
 XX

PS Disclosure; Page 12; 44pp; English.
 PS

XX Example 1 describes the determination of the presence of a mutation
 CC in the pro-alpha(III) gene. Primers used in PCR are given in
 CC AAQ30834-48.
 CC

XX Sequence 29 BP; 5 A; 10 C; 7 G; 7 T; 0 other;
 SQ

Query Match 72.2%; Score 13; DB 13; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ctctctggaagccc 18
 |||||
 Db 11 ctctctggaagccc 23

RESULT 11

AAV83186
 ID AAV83186 standard; DNA; 29 BP.
 XX

XX AAV83186;
 AC

XX 02-MAR-1999 (first entry)
 DT

XX Primer for amplifying GM-CSF cDNA.
 DE

XX Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
 KW immunomodulator; vector; vaccine; cancer; HIV; Leishmania;
 KW Mycobacterium; listeria; Plasmodium; retrovirus; evaluation;
 KW human immunodeficiency virus; PCR primer; ss.
 XX

OS Synthetic.
 OS

PN WO9844788-A2.
 PN

XX 15-OCT-1998.
 PD

XX 09-APR-1998; 98WO-US06944.
 PF

XX 09-DEC-1997; 97US-0069163.
 PR

XX 09-APR-1997; 97US-0838702.
 PR

XX 01-MAY-1997; 97US-0848760.
 PR

XX (CHAN/) CHANG L.
 PA

XX Chang L;
 PI

XX

DR WPI; 1999-024005/02.
 XX Use of immunodeficient mice comprising human cells - particularly
 PT SCID/beige mice comprising human immune cells for evaluating
 PT vaccines against cancers or human pathogens, e.g. HIV
 XX
 PS Example 1b; Page 36; 154pp; English.
 XX
 CC Immunodeficient mice comprising human cells can be used for
 CC exposure to human pathogens and/or their components or human
 CC tumour cells and human peripheral blood lymphocytes. Also claimed
 CC is a vaccine comprising a cell modified to express an antigen and
 CC an immune-modulating protein, this is preferably an expression
 CC vector comprising a polynucleotide sequence that encodes the
 CC antigen and immune-modulating protein. Such vectors can be used
 CC to treat a subject having a tumour by transferring the expression
 CC vector into the tumour so that the antigen and the immune-modulator
 CC are expressed by at least the tumour. The methods can be used for
 CC producing and evaluating vaccines including cancer vaccines and
 CC vaccines directed against human pathogens, e.g. HIV, Leishmania,
 CC Mycobacterium, Listeria or Plasmodium. This sequence is an
 CC intermediate retroviral vector derived from pNL6, a vector approved
 CC for clinical use in the United States. pNL6 is essentially pNL6
 CC digested with ClaI and BclI to remove cloning sites and the pNL6
 CC internal SmaI gene. These were replaced with a polylinker. A neo
 CC gene was then inserted under the transcriptional control of the SV40
 CC enhancer/promoter to create the vector pLSN. Two primers (AAV83185,
 CC AAV83186) were used to amplify the granulocyte macrophage colony
 CC stimulating factor (GM-CSF) cDNA (AAV83189) for its insertion into
 CC pLSN.
 XX
 SQ Sequence 29 BP; 6 A; 9 C; 6 G; 8 T; 0 other;

Query Match 72.2%; Score 13; DB 20; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcactcctgga 13
 |||||
 Db 10 tatcactcctgga 22

RESULT 12
 AA131049/C
 ID AA131049 standard; DNA; 31 BP.
 XX
 AC AA131049;
 XX
 DT 18-OCT-2001 (first entry)
 XX
 DE Human single nucleotide polymorphism (SNP) MUT 2.
 XX
 KW Human; resequence; genotype; disease; forensic; paternity testing;
 KW single nucleotide polymorphism; SNP; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(16,T)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200166800-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-US07268.
 XX
 PR 07-MAR-2000; 2000US-0187510.
 PR 22-MAY-2000; 2000US-0206129.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2001-522952/57.
 XX
 PT Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or
 PT severity of a particular phenotype or disorder (e.g. diabetes)
 PT associated with a particular genotype -
 XX
 PS Claim 1; Page 125; 145pp; English.
 XX
 CC The invention relates to the identification of nucleic acid molecules
 CC (AA129513-AA131314) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing.
 XX
 SQ Sequence 31 BP; 10 A; 7 C; 7 G; 7 T; 0 other;

Query Match 72.2%; Score 13; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tcaactcctggaag 15
 |||||
 Db 25 TCACCTCCTGGAAG 13

RESULT 13
 AAS45602
 ID AAS45602 standard; DNA; 20 BP.

XX
 AC AAS45602;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Mouse GAPDH RT-PCR reverse primer.
 XX
 KW Human; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
 KW cytosolic; neurotropic; neuroprotective; antiinflammatory; antidiabetic;
 KW immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
 KW oxidative stress; neurological disorder; parkinsonism; apoptosis;
 KW meningitis-associated intracranial complication; ischaemia; PCR primer;
 KW inflammatory disorder; autoimmune disorder; arthritis; diabetes;
 KW GAPDH; glyceraldehyde phosphate dehydrogenase.
 XX
 OS Mus musculus.
 XX
 PN WO200164955-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US06572.
 XX
 PR 02-MAR-2000; 2000US-0517467.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Popoff I, Cowser LM;
 XX
 DR WPI; 2001-602570/68.
 XX
 PT Antisense compound useful for treating hyperproliferative,
 PT neurological, inflammatory and autoimmune disorders and diabetes
 PT inhibits human PARP -
 XX
 PS Example 13; Page 80; 168pp; English.

XX The invention relates to antisense oligonucleotides targeted to human
 CC PARG nucleic acid and inhibiting expression of human PARG. PARG
 CC (Poly (ADP-ribose) polymerase plays an important role in chromatin
 CC decondensation, DNA replication, DNA repair, gene expression, malignant
 CC transformation, cellular differentiation and apoptosis. The antisense
 CC oligonucleotide inhibitors are useful for inhibiting the expression of
 CC PARG in human cells or tissues. They are also useful for treating a
 CC human with a disease associated with PARG especially hyperproliferative
 CC disorders (e.g. cancer), cellular injury resulting from oxidative stress,
 CC neurological (e.g. parkinsonism, meningitis-associated intracranial
 CC complications and ischaemia), inflammatory and autoimmune disorders (e.g.
 CC arthritis and diabetes). The present sequence is an RT-PCR (reverse
 CC transcriptase PCR) primer designed to amplify GAPDH (glyceraldehyde
 CC phosphate dehydrogenase) as a control in an experiment to quantitate
 CC PARG mRNA levels.
 XX
 SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 other;
 Query Match 71.1%; Score 12.8; DB 22; Length 20;
 Best Local Similarity 87.5%; Pred. No. 3.2e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 tatcactctctggaagc 16
 Db 4 tctcgctctctggaagc 19
 RESULT 14
 ID AAS21535
 XX AAS21535 standard; DNA; 20 BP.
 AC AAS21535;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Mouse GAPDH reverse PCR primer.
 XX
 KW Survivin; human; mouse; cytostatic; antisense oligonucleotide;
 KW hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200157059-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US02939.
 XX
 PR 02-FEB-2000; 2000US-0496694.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Ackermann EU, Swayze EE, Cowdery LM;
 XX
 DR WPI; 2001-488863/53.
 XX
 PT Novel antisense compounds for modulating the expression of Survivin and
 PT treatment of cancer -
 XX
 PS Example 13; Page 51; 120pp; English.
 XX
 CC The invention relates to antisense oligonucleotides targeted to a nucleic
 CC acid molecule encoding human Survivin, where the antisense
 CC oligonucleotide inhibits the expression of human Survivin. These
 CC antisense oligonucleotides are used in the treatment of an animal
 CC suffering from a disease or condition associated with Survivin, e.g. a
 CC hyperproliferative condition such as cancer, and comprises administering
 CC a therapeutically or prophylactically effective amount of the antisense
 CC oligonucleotide so that expression of Survivin is inhibited. The
 CC oligonucleotides can also be used to treat a human suffering from a
 CC disease or condition characterised by a reduction in apoptosis

CC comprising administering the antisense oligonucleotide to a human. In
 CC addition, the antisense oligonucleotide and a cytotoxic chemotherapeutic
 CC agent e.g. taxol or cisplatin, can be used to modulate apoptosis,
 CC cytokinesis or the cell cycle, or inhibit the proliferation in a cancer
 CC cell by contacting the cell with the antisense oligonucleotide.
 CC AAS21531-AAS21768 represent Survivin nucleic acids, and antisense
 CC oligonucleotides targeted to Survivin, used in the method of the
 CC invention.
 XX
 SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 other;
 Query Match 71.1%; Score 12.8; DB 22; Length 20;
 Best Local Similarity 87.5%; Pred. No. 3.2e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 tatcactctctggaagc 16
 Db 4 tctcgctctctggaagc 19
 RESULT 15
 ID AAS10515
 XX AAS10515 standard; DNA; 20 BP.
 AC AAS10515;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Mouse GAPDH reverse PCR primer.
 XX
 KW Mouse; caspase 3; apoptosis; GAPDH; PCR primer; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200153310-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 11-JAN-2001; 2001WO-US00888.
 XX
 PR 18-JAN-2000; 2000US-0484617.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Zhang H, Cowdery LM;
 XX
 DR WPI; 2001-442252/47.
 XX
 PT New antisense compound to inhibit caspase 3 is useful for treating
 PT hepatitis and atherosclerosis -
 XX
 PS Example 13; Page 81; 127pp; English.
 XX
 CC The present sequence for mouse GAPDH reverse PCR primer is used
 CC with the forward PCR primer (AAS10514) to amplify DNA encoding
 CC mouse GAPDH. The present sequence is described in an invention
 CC relating to novel antisense oligonucleotides (AAS10517-AAS10676)
 CC and methods of using these compounds for the modulation of caspase 3
 CC expression. The caspase 3 antisense oligonucleotides specifically
 CC hybridise with and inhibit the expression of caspase 3. Antisense
 CC compounds targeted to caspase 3 are useful to inhibit caspase 3
 CC expression in cells or tissues and to modulate apoptosis. The caspase 3
 CC antisense oligonucleotides are useful for treating disorders associated
 CC with expression of caspase 3. Such disorders include hyperproliferative
 CC disorders (e.g. cancer), viral infections (e.g. hepatitis),
 CC haematopoietic disorders, autoimmune disorders, atherosclerosis and
 CC neurological disorders (e.g. Alzheimer's disease).
 XX
 SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 other;
 Query Match 71.1%; Score 12.8; DB 22; Length 20;

Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcaactcctggaagc 16
| | | | | | | | | |
Db 4 tctcgcctcctggaagc 19

Search completed: October 12, 2002, 17:08:00
Job time: 9745 sec

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 14:24:45 ; Search time 191.26 seconds
(without alignments) 23.117 Million cell updates/sec

Title: US-09-945-131-1

Perfect score: 18

Sequence: 1 tatcactctctggaagccc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	13.2	73.3	31	2	US-08-821-782-10
c 2	13.2	73.3	31	4	US-09-292-435A-10
3	13	72.2	29	4	US-08-848-760B-7
4	12.8	71.1	20	4	US-09-490-692-15
5	12.8	71.1	20	4	US-09-488-671-15
6	12.8	71.1	20	4	US-09-487-445-15
7	12.8	71.1	20	4	US-09-593-711A-15
8	12.8	71.1	20	4	US-09-484-617-15
9	12.8	71.1	20	4	US-09-721-822A-15
10	12.8	71.1	20	4	US-09-593-589-15
11	12.8	71.1	20	4	US-09-496-694B-15
12	12.8	71.1	26	2	US-08-859-998-18
13	12.8	71.1	26	4	US-08-859-998-18
14	12.4	68.9	17	4	US-08-679-645-214
15	12.4	68.9	18	1	US-08-399-986B-27
16	12.4	68.9	18	1	US-08-493-754A-27
17	12.4	68.9	31	4	US-08-679-645-452
c 18	12.4	68.9	45	2	US-08-596-387B-75
c 19	12.4	68.9	45	2	US-08-596-387B-83
c 20	12.4	68.9	45	4	US-09-067-615-75
c 21	12.4	68.9	45	4	US-09-067-615-83
c 22	12.4	68.9	45	5	PCT-US95-09816A-75
c 23	12.4	68.9	45	5	PCT-US95-09816A-83
c 24	12.2	67.8	40	3	US-09-286-904-58
25	12.2	67.8	31	2	US-08-859-998-202
26	12.2	67.8	31	4	US-09-225-928-202
c 27	12.2	67.8	46	1	US-08-171-389-80

c 28	12.2	67.8	46	1	US-08-123-936-80	Sequence 80, Appl
c 29	12.2	67.8	46	2	US-08-475-228A-80	Sequence 80, Appl
c 30	12.2	67.8	46	3	US-08-482-080A-80	Sequence 80, Appl
c 31	12.2	67.8	46	5	PCT-US93-12388-80	Sequence 80, Appl
32	12	66.7	30	1	US-08-154-019-10	Sequence 10, Appl
33	12	66.7	30	1	US-08-461-333-10	Sequence 10, Appl
34	12	66.7	30	3	US-08-464-167-10	Sequence 10, Appl
35	12	66.7	30	3	US-09-158-313-10	Sequence 10, Appl
36	12	66.7	30	3	US-08-476-798-10	Sequence 10, Appl
37	11.8	65.6	20	3	US-09-280-799-38	Sequence 38, Appl
c 38	11.8	65.6	24	1	US-08-158-682A-7	Sequence 7, Appl
39	11.8	65.6	25	4	US-08-928-465-7	Sequence 7, Appl
c 40	11.8	65.6	30	1	US-08-121-053-17	Sequence 17, Appl
c 41	11.8	65.6	30	1	US-08-455-063-17	Sequence 17, Appl
c 42	11.8	65.6	32	3	US-08-907-468-1	Sequence 1, Appl
c 43	11.8	65.6	37	4	US-09-481-288-12	Sequence 12, Appl
c 44	11.6	64.4	20	1	US-08-449-045C-32	Sequence 32, Appl
c 45	11.6	64.4	20	2	US-08-435-605A-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-821-782-10/c
; Sequence 10, Application US/08821782
; Patent No. 5981183
; GENERAL INFORMATION:
; APPLICANT: Yutaka, Takarada
; APPLICANT: Hiroaki, Inoue
; APPLICANT: Shuji, Shibata
; APPLICANT: Yoshihisa, Kawamura
; TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
; TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING THERMOSTABLE ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 61601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: Dos 5.0
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,782
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ahern, Paul L.
; REGISTRATION NUMBER: 17020
; REFERENCE/DOCKET NUMBER: 66425
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: (25)3533
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-08-821-782-10

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 5

US-09-488-671-15

; Sequence 15, Application US/09488671A

; Patent No. 6187545

; GENERAL INFORMATION:

; APPLICANT: Robert McKay

; APPLICANT: Madeline M. Butler

; APPLICANT: Jacqueline Wyatt

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION

; FILE REFERENCE: RTS-0123

; CURRENT APPLICATION NUMBER: US/09/488,671A

; CURRENT FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 177

; SEQ ID NO 15

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: PCR Primer

US-09-488-671-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;

Best Local Similarity 87.5%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 6

US-09-487-445-15

; Sequence 15, Application US/09487445

; Patent No. 6258600

; GENERAL INFORMATION:

; APPLICANT: Hong Zhang

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION

; FILE REFERENCE: RTS-0107

; CURRENT APPLICATION NUMBER: US/09/487,445

; CURRENT FILING DATE: 2000-01-19

; NUMBER OF SEQ ID NOS: 176

; SEQ ID NO 15

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: PCR Primer

US-09-487-445-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;

Best Local Similarity 87.5%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 7

US-09-593-711A-15

; Sequence 15, Application US/09593711A

; Patent No. 6271030

; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-593-711A-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;

Best Local Similarity 87.5%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 8

US-09-484-617-15

; Sequence 15, Application US/09484617

; Patent No. 6303374

; GENERAL INFORMATION:

; APPLICANT: Hong Zhang

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION

; FILE REFERENCE: RTS-0103

; CURRENT APPLICATION NUMBER: US/09/484,617

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 176

; SEQ ID NO 15

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: PCR Primer

US-09-484-617-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;

Best Local Similarity 87.5%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 9

US-09-721-822A-15

; Sequence 15, Application US/09721822A

; Patent No. 6306606

; GENERAL INFORMATION:

; APPLICANT: Michael J. Weber

; APPLICANT: Jacqueline Wyatt

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF MP-1 EXPRESSION

; FILE REFERENCE: RTS-0142

; CURRENT APPLICATION NUMBER: US/09/721,822A

; CURRENT FILING DATE: 2000-11-22

; NUMBER OF SEQ ID NOS: 135

; SEQ ID NO 15

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-721-822A-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
DB 4 tctcgtctctggaagc 19

RESULT 10
US-09-593-589-15
; Sequence 15, Application US/09593589
; Patent No. 6306655
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP ALPHA EXPRESSION
; FILE REFERENCE: RTS-0119
; CURRENT APPLICATION NUMBER: US/09/593,589
; CURRENT FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-593-589-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
DB 4 tctcgtctctggaagc 19

RESULT 11
US-09-496-694B-15
; Sequence 15, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swazy
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-496-694B-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | | | | | | | |
DB 4 tctcgtctctggaagc 19

RESULT 12
US-08-859-998-18/c
; Sequence 18, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
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; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-18

Query Match 71.1%; Score 12.8; DB 2; Length 26;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
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DB 22 TATGACACCTGGAAGC 7

RESULT 13
US-09-225-928-18/c
; Sequence 18, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex


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;
;   Jokhadze, George
;   Bibilashvili, Robert
;   TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;   EXPRESSION
;   NUMBER OF SEQUENCES: 1375
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 2200 Sand Hill Road, Suite 100
;   CITY: Menlo Park
;   STATE: CA
;   COUNTRY: US
;   ZIP: 94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSeq for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/225,928
;   FILING DATE: 05-Jan-1999
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/859,998
;   FILING DATE: 21-MAY-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Field, Bret E.
;   REGISTRATION NUMBER: 37,620
;   REFERENCE/DOCKET NUMBER: 09096/002001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-322-5070
;   TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 18:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 26 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide primer
;   SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-225-928-18

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Query Match      71.1%; Score 12.8; DB 4; Length 26;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 tatcactctctggaagc 16
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Db 22 TATGACACCTGGAAGC 7

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RESULT 14
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; Sequence 214, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

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;   STREET: 633 West Fifth Street
;   STREET: Suite 4700
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: U.S.A.
;   ZIP: 90071-2066
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   MEDIUM TYPE: storage
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: IBM P.C. DOS 5.0
;   SOFTWARE: Word Perfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/679,645
;   FILING DATE: July 12, 1996
;   CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/001,135
;   FILING DATE: July 13, 1995
;   APPLICATION NUMBER: 08/300,726
;   FILING DATE: September 2, 1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Warburg, Richard J.
;   REGISTRATION NUMBER: 32,327
;   REFERENCE/DOCKET NUMBER: 219/247
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 489-1600
;   TELEFAX: (213) 955-0440
;   TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 214:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   US-08-679-645-214

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Query Match      68.9%; Score 12.4; DB 4; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 atcactctctggaag 15
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Db 3 AUCUCUCCUGGAAG 16

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RESULT 15
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; Sequence 27, Application US/08399986B
; Patent No. 5801041
; GENERAL INFORMATION:
; APPLICANT: Godwin, Andrew K.
; TITLE OF INVENTION: No. 5801041el Gene Associated with Suppression
; TITLE OF INVENTION: of Tumor Development
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,986B
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

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; NAME: Hagan, Patrick J.
; REGISTRATION NUMBER: 27,643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-399-986B-27

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Query Match      68.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 3 tcactcctggaagc 16
   || |||||
Db 5 TCCCTCCTGGAAGC 18

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Search completed: October 12, 2002, 16:54:34
Job time: 8989 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:09:10 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-1

Perfect score: 18

Sequence: 1 tatcactctctggaagccc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	16	US-09-241-561-1	Sequence 1, Appli
2	15.4	85.6	25	35	US-09-954-427-302324	Sequence 302324,
3	15.4	85.6	25	62	US-60-233-166-302324	Sequence 302324,
4	14.8	82.2	25	74	US-60-353-987-128993	Sequence 128993,
5	14.4	80.0	25	17	US-09-396-196F-69451	Sequence 69450, A
6	14.4	80.0	25	17	US-09-396-196F-69451	Sequence 69451, A
7	13.8	76.7	25	35	US-09-954-427-98726	Sequence 98726, A
8	13.8	76.7	25	35	US-09-954-427-253488	Sequence 253488,
9	13.8	76.7	25	62	US-60-233-166-98726	Sequence 98726, A
10	13.8	76.7	25	62	US-60-233-166-253488	Sequence 253488,
11	13.8	76.7	25	74	US-60-353-987-358641	Sequence 358641,
12	13.8	76.7	25	74	US-60-353-987-614848	Sequence 614848,
13	13.4	74.4	25	26	US-09-660-220-110931	Sequence 110931,
14	13.4	74.4	25	35	US-09-954-427-162374	Sequence 162374,
15	13.4	74.4	25	35	US-09-954-427-162386	Sequence 162386,
16	13.4	74.4	25	35	US-09-956-584-185260	Sequence 185260,
17	13.4	74.4	25	35	US-09-956-584-318707	Sequence 318707,
18	13.4	74.4	25	35	US-09-956-584-362472	Sequence 362472,
19	13.4	74.4	25	62	US-60-233-166-162374	Sequence 162374,
20	13.4	74.4	25	62	US-60-233-166-162386	Sequence 162386,
21	13.4	74.4	25	62	US-60-234-017-153617	Sequence 153617,
22	13.4	74.4	25	62	US-60-234-017-280338	Sequence 280338,
23	13.4	74.4	25	62	US-60-234-017-355634	Sequence 355634,
24	13.2	73.3	25	26	US-09-660-220-66859	Sequence 66859, A
25	13.2	73.3	25	26	US-09-660-247-719	Sequence 719, App
26	13.2	73.3	25	26	US-09-660-247-723	Sequence 723, App
27	13.2	73.3	25	35	US-09-954-427-349744	Sequence 349744,
28	13.2	73.3	25	35	US-09-956-584-88931	Sequence 88931, A
29	13.2	73.3	25	35	US-09-956-584-122601	Sequence 122601,
30	13.2	73.3	25	62	US-60-232-638-876	Sequence 876, App
31	13.2	73.3	25	62	US-60-232-638-887	Sequence 887, App

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34 13.2 73.3 25 62 US-60-234-017-122761 Sequence 122761,
35 13.2 73.3 25 74 US-60-353-987-106006 Sequence 106006,
36 13.2 73.3 25 74 US-60-353-987-128994 Sequence 128994,
c 37 13.2 73.3 25 74 US-60-353-987-183963 Sequence 183963,
38 13.2 73.3 25 74 US-60-353-987-630598 Sequence 630598,
c 39 13.2 73.3 25 74 US-60-353-987-831273 Sequence 831273,
c 40 13.2 73.3 31 8 US-08-446-709A-10 Sequence 10, Appli
41 13 72.2 25 17 US-09-396-196F-41662 Sequence 41662, A
42 13 72.2 25 17 US-09-396-196F-41663 Sequence 41663, A
43 13 72.2 25 17 US-09-396-196F-41664 Sequence 41664, A
44 13 72.2 29 4 US-08-085-252-2 Sequence 2, Appli
45 13 72.2 29 12 US-08-838-702-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-241-561-1
; Sequence 1, Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-1

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tatcaactcctggaagcc 18
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Db 1 tatcaactcctggaagcc 18

RESULT 2
US-09-954-427-302324
; Sequence 302324, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 302324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AJ223184
US-09-954-427-302324
Query Match 85.6%; Score 15.4; DB 35; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 tatcaactcctggaagcc 17
| | | | | | | | | | | | | | | | | |
Db 8 tatcaactcctggaagac 24
RESULT 3
US-60-233-166-302324
; Sequence 302324, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0.
; SEQ ID NO 302324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AJ223184
US-60-233-166-302324

Query Match 85.6%; Score 15.4; DB 62; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 tatcaactcctggaagcc 17
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Db 8 tatcaactcctggaagac 24

RESULT 4
US-60-353-987-128993
; Sequence 128993, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 128993
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-128993

Query Match 82.2%; Score 14.8; DB 74; Length 25;
Best Local Similarity 88.9%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tatcaactcctggaagcc 18
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Db 6 tgcactcctggaagtc 23
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US-09-396-196F-69450
; Sequence 69450, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69450
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-69450

Query Match 80.0%; Score 14.4; DB 17; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactctctggaagccc 18
Db 4 tcactctctggaagccc 19

RESULT 6
US-09-396-196F-69451
; Sequence 69451, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69451
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-69451

Query Match 80.0%; Score 14.4; DB 17; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactctctggaagccc 18
Db 1 tcactctctggaagccc 16

RESULT 7
US-09-954-427-98726/c
; Sequence 98726, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427

; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98726
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA858718
US-09-954-427-98726

Query Match 76.7%; Score 13.8; DB 35; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagccc 17
Db 22 TATCACCCTGTGAAGCC 6

RESULT 8
US-09-954-427-253488
; Sequence 253488, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI044232
US-09-954-427-253488

Query Match 76.7%; Score 13.8; DB 35; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcactctctggaagccc 18
Db 1 atcactactggaagctc 17

RESULT 9
US-60-233-166-98726/c
; Sequence 98726, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98726
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA858718
US-60-233-166-98726

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Query Match          76.7%; Score 13.8; DB 62; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatactctctggaagcc 17
    ||||| ||||| |||
Db 22 TATCACCGTGGAAAGCC 6

RESULT 10
US-60-233-166-253488
; Sequence 253488, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 200907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI044232
US-60-233-166-253488

Query Match          76.7%; Score 13.8; DB 62; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcactctctggaagcc 18
    ||||| ||||| |||
Db 1 atcactactggaagctc 17

RESULT 11
US-60-353-987-358641/c
; Sequence 358641, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 358641
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-358641

Query Match          76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcactctctggaagcc 18
    ||||| ||||| |||
Db 22 ATCACTCTGGTGGCC 6

RESULT 12
US-60-353-987-614848/c
; Sequence 614848, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 614848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-614848

Query Match          76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatactctctggaagcc 17
    ||||| ||||| |||
Db 17 TGTCACTCTCTGGAATCC 1

RESULT 13
US-09-660-220-110931
; Sequence 110931, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: US/09/660,220
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110931
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X03066
US-09-660-220-110931

Query Match          74.4%; Score 13.4; DB 26; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
    ||||| ||||| |||
Db 7 atcactctctggaatc 21

RESULT 14
US-09-954-427-162374/c
; Sequence 162374, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162374
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA925104
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Search completed: October 12, 2002, 20:42:28
Job time: 16398 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 14:27:25 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-1

Perfect score: 18

Sequence: 1 tatcactctctggaagccc 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New.*

1: /cgn2_6/ptodata/1/pna/pct_NEW_COMB.seq.*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*

5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*

6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*

7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*

8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	18	100.0	18	5	US-09-945-131-1		Sequence 1, Appli
2	14.4	80.0	25	5	US-09-396-196G-69450		Sequence 69450, A
3	14.4	80.0	25	5	US-09-396-196G-69451		Sequence 69451, A
4	13.4	74.4	17	5	US-09-780-164-65		Sequence 65, Appl
5	13.4	74.4	17	5	US-09-780-164-441		Sequence 441, App
6	13.4	74.4	17	5	US-09-780-164-442		Sequence 442, App
7	13.2	73.3	25	6	US-10-215-112-2937		Sequence 2937, Ap
8	13.2	73.3	25	6	US-10-215-112-7753		Sequence 7753, Ap
9	13	72.2	25	5	US-09-396-196G-41662		Sequence 41662, A
10	13	72.2	25	5	US-09-396-196G-41663		Sequence 41663, A
11	13	72.2	25	5	US-09-396-196G-41664		Sequence 41664, A
12	12.8	71.1	20	1	PCT-US02-22672-15		Sequence 15, Appl
13	12.8	71.1	20	5	US-09-666-269B-8		Sequence 8, Appli
14	12.8	71.1	20	6	US-10-181-107-15		Sequence 15, Appl
15	12.8	71.1	20	6	US-10-181-177-15		Sequence 15, Appl
16	12.8	71.1	20	6	US-10-181-316-15		Sequence 15, Appl
17	12.8	71.1	20	6	US-10-181-542-15		Sequence 15, Appl
18	12.8	71.1	20	6	US-10-181-846-15		Sequence 15, Appl
19	12.8	71.1	20	6	US-10-182-049-15		Sequence 15, Appl
20	12.8	71.1	23	6	US-10-188-777-6		Sequence 6, Appli
21	12.8	71.1	25	5	US-09-396-196G-56409		Sequence 56409, A
22	12.8	71.1	25	5	US-09-396-196G-56426		Sequence 56426, A
23	12.8	71.1	25	5	US-09-396-196G-80096		Sequence 80096, A
24	12.8	71.1	26	5	US-09-225-201B-18		Sequence 18, Appl
25	12.4	68.9	17	5	US-09-780-164-440		Sequence 440, App

26 12.4 68.9 17 5 US-09-780-164-1001 Sequence 1001, Ap
27 12.4 68.9 25 5 US-09-956-604-57406 Sequence 57406, A
28 12.4 68.9 25 5 US-09-956-604-57407 Sequence 57407, A
29 12.4 68.9 25 5 US-09-956-604-57408 Sequence 57408, A
30 12.4 68.9 25 5 US-09-956-604-57415 Sequence 57415, A
31 12.4 68.9 25 5 US-09-956-604-57434 Sequence 57434, A
32 12.4 68.9 25 5 US-09-956-604-57436 Sequence 57436, A
33 12.4 68.9 25 5 US-09-956-604-57440 Sequence 57440, A
34 12.4 68.9 25 5 US-09-956-604-57441 Sequence 57441, A
35 12.4 68.9 25 5 US-09-956-604-57442 Sequence 57442, A
36 12.4 68.9 25 5 US-09-956-604-57443 Sequence 57443, A
c 37 12.4 68.9 25 5 US-09-956-604-57475 Sequence 57475, A
c 38 12.4 68.9 25 5 US-09-956-604-57476 Sequence 57476, A
c 39 12.4 68.9 25 5 US-09-956-604-57478 Sequence 57478, A
c 40 12.4 68.9 25 5 US-09-956-604-57479 Sequence 57479, A
c 41 12.4 68.9 25 5 US-09-956-604-57481 Sequence 57481, A
c 42 12.4 68.9 25 5 US-09-956-604-57482 Sequence 57482, A
c 43 12.4 68.9 25 5 US-09-956-604-57485 Sequence 57485, A
44 12.4 68.9 25 5 US-09-396-196G-37587 Sequence 37587, A
45 12.4 68.9 25 5 US-09-396-196G-37588 Sequence 37588, A

ALIGNMENTS

RESULT 1

US-09-945-131-1

; Sequence 1, Application US/09945131

; GENERAL INFORMATION:

; APPLICANT: SIROIS, Martin G.

; APPLICANT: EDELMAN, Elazer R.

; APPLICANT: ROSENBERG, Robert D.

; APPLICANT: SIMONS, Michael

; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing

; TITLE OF INVENTION: Restenosis

; FILE REFERENCE: 12554.4

; CURRENT APPLICATION NUMBER: US/09/945,131

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Rattus rattus

; FEATURE:

; NAME/KEY: mRNA

; LOCATION: (1)..(18)

; OTHER INFORMATION: Antisense oligonucleotide

US-09-945-131-1

Query Match 100.0% Score 18; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcactctctggaagccc 18

|||||

Db 1 tatcactctctggaagccc 18

RESULT 2

US-09-396-196G-69450

; Sequence 69450, Application US/09396196G

; GENERAL INFORMATION:

; APPLICANT: Michael Mitmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69450
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-69450

Query Match 80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactctctggaagccc 18
||||| |||||||||
Db 4 tcactctctggaagccc 19

RESULT 3
US-09-396-196G-69451
; Sequence 69451, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69451
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-69451

Query Match 80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactctctggaagccc 18
||||| |||||||||
Db 1 tcactctctggaagccc 16

RESULT 4
US-09-780-164-65
; Sequence 65, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 17
; TYPE: RNA

; ORGANISM: Homo sapiens
US-09-780-164-65

Query Match 74.4%; Score 13.4; DB 5; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.7e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
|:||||:|||||
Db 3 acaacuccuggcagc 17

RESULT 5
US-09-780-164-441
; Sequence 441, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 441
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-441

Query Match 74.4%; Score 13.4; DB 5; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.7e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
|:||||:|||||
Db 2 acaacuccuggcagc 16

RESULT 6
US-09-780-164-442
; Sequence 442, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 442
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-442

Query Match 74.4%; Score 13.4; DB 5; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.7e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
|:||||:|||||
Db 1 acaacuccuggcagc 15

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; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41662
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-41662

Query Match          72.2%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcaactcctgga 13
Db 11 tatcaactcctgga 23

RESULT 10
US-09-396-196G-41663
; Sequence 41663, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41663
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-41663

Query Match          72.2%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcaactcctgga 13
Db 8 tatcaactcctgga 20

RESULT 11
US-09-396-196G-41664
; Sequence 41664, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-41664

US-10-215-112-2937
; Sequence 2937, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2937

Query Match          73.3%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcaactcctggaagccc 18
Db 5 tatcaactcctggaagctc 22

RESULT 8
US-10-215-112-7753
; Sequence 7753, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-7753

Query Match          73.3%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcaactcctggaagccc 18
Db 1 tatcaactcctggaagctc 18

RESULT 9
US-09-396-196G-41662
; Sequence 41662, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
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US-09-396-196G-41664

Query Match 72.2%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcaactcctgga 13
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Db 2 tatcaactcctgga 14

RESULT 12
PCT-US02-22672-15
; Sequence 15, Application PC/TUS0222672
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Madeline M. Butler
; APPLICANT: Andrew T. Watt
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
; FILE REFERENCE: ISPH-0693
; CURRENT APPLICATION NUMBER: PCT/US02/22672
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/915,814
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
PCT-US02-22672-15

Query Match 71.1%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactcctggaagc 16
| | | | | | | | | |
Db 4 tctcgctcctggaagc 19

RESULT 13
US-09-666-269B-8
; Sequence 8, Application US/09666269B
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: C. Frank Bennett
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; APPLICANT: William Ricketts
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF FLIP-C EXPRESSION
; FILE REFERENCE: RTS-0202
; CURRENT APPLICATION NUMBER: US/09/666,269B
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 133
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-666-269B-8

Query Match 71.1%; Score 12.8; DB 5; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactcctggaagc 16
| | | | | | | | | |
Db 4 tctcgctcctggaagc 19

RESULT 14
US-10-181-107-15
; Sequence 15, Application US/10181107
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
; FILE REFERENCE: RTSP-0325
; CURRENT APPLICATION NUMBER: US/10/181,107
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: PCT/US01/00888
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 09/484,617
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-181-107-15

Query Match 71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactcctggaagc 16
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Db 4 tctcgctcctggaagc 19

RESULT 15
US-10-181-177-15
; Sequence 15, Application US/10181177
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
; FILE REFERENCE: RTSP-0334
; CURRENT APPLICATION NUMBER: US/10/181,177
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/00955
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 09/487,445
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-181-177-15

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Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactcctggaagc 16
| | | | | | | | | |
Db 4 tctcgctcctggaagc 19

Search completed: October 12, 2002, 17:27:27
Job time: 10802 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:51:10 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18

Sequence: 1 tctgagcactaaagctgg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

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6: gb_pat.*

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8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

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28: em_un.*

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32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description

1	13.2	73.3	19	6	AX079136	AX079136 Sequence
2	13.2	73.3	24	6	AX196752	AX196752 Sequence
3	13.2	73.3	24	6	AX196754	AX196754 Sequence
c 4	12.4	68.9	27	6	AX116019	AX116019 Sequence
c 5	12.2	67.8	21	6	AX353507	AX353507 Sequence
c 6	12	66.7	39	6	AX207258	AX207258 Sequence
c 7	11.8	65.6	20	6	AX175139	AX175139 Sequence
c 8	11.8	65.6	20	6	AX175147	AX175147 Sequence
9	11.8	65.6	30	9	HS5B3VB19	X84271 H.sapiens m
10	11.8	65.6	32	6	E14820	E14820 PCR primer
11	11.8	65.6	33	6	AX168196	AX168196 Sequence
c 12	11.8	65.6	34	6	A40268	A40268 Sequence 8
c 13	11.8	65.6	45	6	A11864	A11864 Nucleotide
14	11.8	65.6	48	9	HSA010889	AJ010889 Homo sapi
c 15	11.8	65.6	50	9	AF057502	AF057502 Homo sapi
c 16	11.6	64.4	24	6	AX138596	AX138596 Sequence
c 17	11.6	64.4	26	6	AX049166	AX049166 Sequence
c 18	11.6	64.4	26	6	AX049771	AX049771 Sequence
c 19	11.6	64.4	26	6	AX050769	AX050769 Sequence
c 20	11.6	64.4	27	6	A50992	A50992 Sequence 33
21	11.6	64.4	30	6	AR021104	AR021104 Sequence
22	11.6	64.4	33	6	A77273	A77273 Sequence 61
c 23	11.6	64.4	34	23	E11247	E11247 PCR primer
c 24	11.6	64.4	35	6	AX001436	AX001436 Sequence
c 25	11.6	64.4	42	10	MMU299488	AJ299488 Mus muscu
c 26	11.4	63.3	22	6	I81225	I81225 Sequence 9
c 27	11.4	63.3	24	6	AX104235	AX104235 Sequence
c 28	11.4	63.3	24	6	AX262438	AX262438 Sequence
c 29	11.4	63.3	24	6	AX355033	AX355033 Sequence
c 30	11.4	63.3	25	6	A22036	A22036 Oligonucleo
31	11.4	63.3	27	9	S81137	S81137 T cell anti
32	11.4	63.3	41	6	AX184259	AX184259 Sequence
33	11.4	63.3	50	6	AX157550	AX157550 Sequence
c 34	11.2	62.2	21	6	AR031042	AR031042 Sequence
35	11.2	62.2	21	6	AX097000	AX097000 Sequence
c 36	11.2	62.2	21	6	AX191211	AX191211 Sequence
c 37	11.2	62.2	21	12	AB069060	AB069060 Synthetic
c 38	11.2	62.2	24	6	AX117122	AX117122 Sequence
39	11.2	62.2	25	6	A35701	A35701 Mutated HRV
c 40	11.2	62.2	25	6	AR109013	AR109013 Sequence
c 41	11.2	62.2	25	6	I05539	I05539 Sequence 5
c 42	11.2	62.2	25	6	I06065	I06065 Sequence 12
43	11.2	62.2	26	6	A34026	A34026 Synthetic P
c 44	11.2	62.2	26	6	A34027	A34027 Synthetic P
45	11.2	62.2	26	6	A77247	A77247 Sequence 35

ALIGNMENTS

RESULT 1	AX079136	AX079136	Sequence 16 from Patent WO0106004.	19 bp	DNA	linear	PAT 22-FEB-2001
LOCUS	AX079136	Sequence 16 from Patent WO0106004.					
DEFINITION	AX079136	AX079136.1	GI:13158709				
ACCESSION	AX079136						
VERSION	AX079136.1						
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
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ORIGIN							

ORIGIN

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Query Match          73.3%; Score 13.2; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18
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Db 1 TCTGACCAACAAGCTGG 18

RESULT 2
LOCUS AX196752 24 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 459 from Patent WO0151627.
ACCESSION AX196752
VERSION AX196752.1 GI:15386958
KEYWORDS soybean.
SOURCE Glycine max
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
TITLE Nucleic acid molecules and other molecules associated with soybean
JOURNAL cyst nematode resistance
PATENT: WO 0151627-A 459 19-JUL-2001;
MONSANTO COMPANY (US)
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Query Match          73.3%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18
    ||||| || ||||| |||
Db 1 TCTGACCAACAAGCTGG 18

RESULT 3
LOCUS AX196754 24 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 461 from Patent WO0151627.
ACCESSION AX196754
VERSION AX196754.1 GI:15386960
KEYWORDS soybean.
SOURCE Glycine max
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
TITLE Nucleic acid molecules and other molecules associated with soybean
JOURNAL cyst nematode resistance
PATENT: WO 0151627-A 461 19-JUL-2001;
MONSANTO COMPANY (US)
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ORIGIN

Query Match          73.3%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18
    ||||| || ||||| |||
Db 1 TCTGACCAACAAGCTGG 18

RESULT 4
LOCUS AX116019 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1142 from Patent WO0129262.
ACCESSION AX116019
VERSION AX116019.1 GI:14032961
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1142 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
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BASE COUNT 9 a 5 c 6 g 7 t
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Best Local Similarity 92.9%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctgagcactaaag 14
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Db 26 TCTGACACTAAG 13

RESULT 5
LOCUS AX353507/c 21 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 39 from Patent WO0204636.
ACCESSION AX353507
VERSION AX353507.1 GI:18618582
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS van Roy,F., Goossens,S., Janssens,B. and Vanpoucke,G.
TITLE Novel _g(a) expressed in heart and testis
JOURNAL Patent: WO 0204636-A 39 17-JAN-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
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            /note="splice acceptor 16"
BASE COUNT 6 a 4 c 4 g 7 t
ORIGIN

Query Match          67.8%; Score 12.2; DB 6; Length 21;
Best Local Similarity 82.4%; Pred. No. 5.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 tctgagcactaaagctg 17
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Db 20 TCTGGGCAATAATG 4

RESULT 6
LOCUS AX207258
DEFINITION Sequence 5 from Patent WO0155366.
ACCESSION AX207258
VERSION AX207258.1 GI:15395041
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Schumacher,A.N. and Kessels,H.W.
TITLE T cell receptor libraries
JOURNAL Patent: WO 0155366-A 5 02-AUG-2001;
          Vereniging Het Nederlands Kanker Instituut (NL)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 6.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 cactaaagctg 18
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Db 39 CACTAAAGCTGG 28

RESULT 7
LOCUS AX175139/c
DEFINITION Sequence 20 from Patent WO0142465.
ACCESSION AX175139
VERSION AX175139.1 GI:14598547
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Nakayama,N., Wen,D., Han,C.Y., He,C. and Yu,D.
TITLE Chordin-like molecules and uses thereof
JOURNAL Patent: WO 0142465-A 20 14-JUN-2001;
          Amgen Inc. (US)
FEATURES
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BASE COUNT 4 a 7 c 4 g 5 t
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Query Match 65.6%; Score 11.8; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 9.6e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 gagcactaaagctg 18
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Db 20 GTGGACTAAAGCTGG 6

RESULT 9
LOCUS HSB3VB19
DEFINITION H.sapiens mRNA for TCR beta chain (clone 5beta3).
ACCESSION X84271
VERSION X84271.1 GI:728570
KEYWORDS Jbeta segment; TCR beta chain; Vbeta segment.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Davodeau,F.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1995) F. Davodeau, INSERM U211, Institut de
          Biologie, 9 Quai Moncousu, 44035 Nantes Cedex, FRANCE
REFERENCE
AUTHORS Davodeau,F., Peyrat,M.A., Romagne,F., Necker,A., Hallet,M.M.,
          Vie,H. and Bonneville,M.
TITLE Dual T cell receptor beta chain expression on human T lymphocytes
JOURNAL J. Exp. Med. 181 (4), 1391-1398 (1995)
MEDLINE 95213664
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Best Local Similarity 86.7%; Pred. No. 9.2e+04;

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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16
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Db 10 CTGAGACTGAAGCT 24

RESULT 10
LOCUS E14820 32 bp DNA linear PAT 28-JUL-1999
DEFINITION PCR primer for gaining rabbit M-CSF gene.
ACCESSION E14820
VERSION E14820.1 GI:5709503
KEYWORDS JP 1998014581-A/4.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Matsuyama,K., Ota,A., Kato,K. and Shimamura,S.
TITLE RABBIT-TYPE MACROPHAGE COLONY STIMULANT FACTOR AND DNA FRAGMENT
CODING THE SAME
JOURNAL Patent: JP 1998014581-A 4 20-JAN-1998;
MORINAGA MILK IND CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1998014581-A/4
PD 20-JAN-1998
PF 08-JUL-1996 JP 1996177916
PI MATSUYAMA KOKI, OTA ATSUSHI, KATO KAYOKO, SHIMAMURA SEIICHI PC
(C12N15/09,C07K14/535,C12N1/21,C12P21/02,C12N1/21,C12R1:19), PC
(C12P21/02,
PC C12R1:19);
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BASE COUNT 8 a 8 c 10 g
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Query Match 65.6%; Score 11.8; DB 6; Length 32;
Best Local Similarity 86.7%; Pred. No. 9.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctgagcactaaagc 15
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Db 17 TCTGAGCAGCTGCAGC 31

RESULT 11
LOCUS AX168196 33 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 36 from Patent WO0142474.
ACCESSION AX168196
VERSION AX168196.1 GI:14597469
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 33)
AUTHORS Welcher,A., Wen,D. and Kelly,M.
TITLE Interferon-like molecules and uses thereof
JOURNAL Patent: WO 0142474-A 36 14-JUN-2001;
Angen Inc. (US)
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BASE COUNT 11 a 11 c 5 g
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Query Match 65.6%; Score 11.8; DB 6; Length 33;
Best Local Similarity 86.7%; Pred. No. 9.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgagcactaaagctg 17
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Db 14 TGAGCACCACCTG 28

RESULT 12
LOCUS A40268/c 34 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 8 from Patent WO9424300.
ACCESSION A40268
VERSION A40268.1 GI:2296364
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 34)
AUTHORS Jacobs,E.
TITLE TRANSCRIPTION ASSEMBLY FOR GENE TRANSFER IN EUKARYOTES
JOURNAL Patent: WO 9424300-A 8 27-OCT-1994;
TRANSGENE SA (FR)
COMMENT Other publication AU 6571994 941108
Other publication FR 2703996 941021
Other publication CA 2160697 941027.
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Query Match 65.6%; Score 11.8; DB 6; Length 34;
Best Local Similarity 86.7%; Pred. No. 9.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16
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Db 21 CAGAGCACTGAAGCT 7

RESULT 13
LOCUS A11864 45 bp mRNA linear PAT 10-JAN-1994
DEFINITION Nucleotide sequence 12 from patent number EP0387775.
ACCESSION A11864
VERSION A11864.1 GI:492543
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Beug,H., Birnstiel,M.L., Cotten,M., Wagner,E. and Kandolf,H.
TITLE Genetic construct for inhibiting RNA function
JOURNAL Patent: EP 0387775-A 12 19-SEP-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H.
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Query Match          65.6%; Score 11.8; DB 6; Length 45;
Best Local Similarity 86.7%; Pred. No. 8.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ttagcactaaagctg 17
    |||| || |||||
Db 25 TGAGGACCAAGCTG 39

RESULT 14
HSA010889
LOCUS      HSA010889      48 bp      mRNA      linear      PRI 02-MAR-1999
DEFINITION Homo sapiens mRNA for T-cell receptor, beta-chain VDJC region,
donor 009 haplotype, A2 A3 B7 B37.
ACCESSION  AJ010889
VERSION     AJ010889.1 GI:3559912
KEYWORDS   beta-chain; T-cell receptor; VDJC region.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 48)
AUTHORS   Weekes,M.P.
TITLE     Direct Submission
JOURNAL   Submitted (04-SEP-1998) Weekes M.P., Department of Medicine,
University of Cambridge Clinical School, Level 5 Box 157,
Addenbrooke's Hospital, Hills Road, Cambridge, CB2 2QQ, UK
REFERENCE  2 (bases 1 to 48)
AUTHORS   Weekes,M.P., Wills,M.R., Mynard,K., Carmichael,A.J. and
Sissons,J.G.
TITLE     The memory cytotoxic T-lymphocyte (CTL) response to human
cytomegalovirus infection contains individual peptide-specific CTL
clones that have undergone extensive expansion in vivo
JOURNAL   J. Virol. 73 (3), 2099-2108 (1999)
MEDLINE   99138992
FEATURES   Location/Qualifiers
            source
            1..48
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /haplotype="A2 A3 B7 B37"
            /sex="Male"
            /tissue_type="blood"
            /cell_type="cytotoxic T-lymphocyte clones"
            /clones="10/97 Clones B56, C56; 02/98 Clones 1a, 1b, 2a"
            <1..>48
            /product="TCRBV14SLBJ1S1 junctional region"
            V_region
            13..25
            N_region
            J_segment
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            BASE COUNT  9 a 14 c 13 g 12 t
            ORIGIN
            1
            25 CTGAACACTGAAGCT 39

Query Match          65.6%; Score 11.8; DB 9; Length 48;
Best Local Similarity 86.7%; Pred. No. 8.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ctgagcactaaagct 16
    |||| |||| |||||
Db 25 CTGAACACTGAAGCT 39

RESULT 15
AF057502/c
LOCUS      AF057502      50 bp      DNA      linear      PRI 01-AUG-1999
DEFINITION Homo sapiens clone C53B Smu-Sgamma4 immunoglobulin switch
recombination junction.
ACCESSION  AF057502
VERSION     AF057502.1 GI:5668863
KEYWORDS   human.
SOURCE     human.

```

```

ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Pan,Q., Rabbani,H. and Hammarstrom,L.
TITLE     Characterization of human gamma 4 switch region polymorphisms
            suggests a meiotic recombinational hot spot within the Ig locus:
            influence of S region length on IgG4 production
JOURNAL   J. Immunol. 161 (7), 3520-3526 (1998)
MEDLINE   98430672
REFERENCE  2 (bases 1 to 50)
AUTHORS   Pan,Q. and Hammarstrom,L.
TITLE     Direct Submission
JOURNAL   Submitted (06-APR-1998) Clinical Immunology, Karolinska Institute,
            Huddinge Hospital, Huddinge S141-86, Sweden
FEATURES   Location/Qualifiers
            source
            1..50
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="14"
            /map="14q32"
            /clone="C53B"
            /note="sequenced from a cloned PCR product"
            misc_feature
            1..50
            /note="Smu-Sgamma4; recombination between the switch Smu
            region and the switch Sgamma4 region"
            /function="immunoglobulin switch recombination junction"
            BASE COUNT  12 a 12 c 20 g 6 t
            ORIGIN
            1
            27 TCTGAGCTCCAAAGC 13

Query Match          65.6%; Score 11.8; DB 9; Length 50;
Best Local Similarity 86.7%; Pred. No. 8.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagc 15
    ||||| |||||
Db 27 TCTGAGCTCCAAAGC 13

Search completed: October 12, 2002, 16:51:13
Job time: 8888 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:00 ; Search time 792.17 seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18

Sequence: 1 tctgagcactaaagctgg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	18	100.0	18	AA13830	Murine PDGFR-beta
2	13.2	73.3	19	AAZ89251	Rat adenosine rece
3	13.2	73.3	19	AAF57945	Low abundance nucl
4	13.2	73.3	21	AAZ74041	Human biallelic ma
5	13.2	73.3	24	AAI61828	Soybean 240017 reg
6	13.2	73.3	24	AAI61830	Soybean 240017 reg
c 7	13	72.2	41	AAZ48359	Primer specific fo
c 8	12.8	71.1	47	AAZ03932	Factor-V NASBA pri
9	12.4	68.9	18	AAZ74877	Human biallelic ma

c 10	12.4	68.9	27	22	AAH38346	SNP specific lower
c 11	12.2	67.8	27	18	AAZ72197	Mouse flk-1 VEGF r
c 12	12.2	67.8	30	20	AAZ12424	PCR primer used to
c 13	12.2	67.8	30	21	AAZ55464	Neisseria species
c 14	12.2	67.8	38	16	AAQ92440	TCR gamma constant
c 15	12	66.7	39	22	AAH43130	Primer: F5-alpha-t
c 16	11.8	65.6	20	22	AAQ08118	Murine chordin-lik
c 17	11.8	65.6	20	22	AAQ08126	Murine chordin-lik
c 18	11.8	65.6	21	21	AAH36864	MM/LGMD2B region p
c 19	11.8	65.6	21	21	AAH11409	Human dysferlin PC
c 20	11.8	65.6	24	21	AAQ01967	Antisense PCR prim
c 21	11.8	65.6	26	22	AAH75969	Human interferon-1
c 22	11.8	65.6	27	13	AAQ25386	PCR primer D for r
c 23	11.8	65.6	28	21	AAZ59472	Poliovirus Sabin s
c 24	11.8	65.6	32	19	AAV12748	Primer for rabbit
c 25	11.8	65.6	33	22	AAQ08270	Human Interferon-L
c 26	11.8	65.6	34	15	AAQ73086	5' primer to ampli
c 27	11.8	65.6	36	20	AAZ08584	Anti-EGFP hammehe
c 28	11.8	65.6	36	20	AAZ78668	Anti-green fluorese
c 29	11.8	65.6	38	21	AAZ60588	PCR primer used to
c 30	11.8	65.6	38	22	AAZ72336	5' PCR Primer used
c 31	11.8	65.6	50	21	AAZ48337	Primer specific fo
c 32	11.6	64.4	24	22	AAZ48283	Human G-CSF forwar
c 33	11.6	64.4	26	22	AAQ99396	Primer #5 used to
c 34	11.6	64.4	26	22	AAZ16817	Human homolog of D
c 35	11.6	64.4	26	22	AAZ17459	Human homolog of D
c 36	11.6	64.4	27	17	AAZ29430	Interleukin-2 gene
c 37	11.6	64.4	27	22	AAZ76152	Human stem cell fa
c 38	11.6	64.4	30	14	AAQ37676	Probe complementar
c 39	11.6	64.4	34	17	AAA40130	Human IL-8 recepto
c 40	11.6	64.4	35	20	AAZ22453	Human CPRM1 DNA ex
c 41	11.6	64.4	38	22	AAZ61942	Polyoma virus vpl
c 42	11.6	64.4	41	20	AAZ19292	Human granulocyte
c 43	11.6	64.4	47	21	AAZ68517	Human map-related
c 44	11.4	63.3	18	22	AAQ09707	Cryptosporidium pa
c 45	11.4	63.3	20	20	AAZ95938	PCR primer used to

ALIGNMENTS

RESULT	1
AA13830	
ID	AA13830 standard; DNA; 18 BP.
XX	
AC	AA13830;
XX	
DT	27-JUL-2000 (first entry)
XX	
DE	Murine PDGFR-beta phosphorothioate antisense oligonucleotide SEQ ID NO:2.
XX	
KW	Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW	PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW	recurrent stenosis; cardiovascular injury; ss.
XX	
OS	Mus sp.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1..18
FT	/*tag= a
XX	/note= "phosphorothioate linkages"
PN	CA2228977-A1.
XX	
PD	07-MAY-1999.
XX	
PF	03-FEB-1998; 98CA-2228977.
XX	
PR	07-NOV-1997; 97CA-2215360.
XX	
PA	(EDEL/) EDELMAN E R.
PA	(ROSE/) ROSENBERG R D.
PA	(SIRO/) SIROIS M G.

PA (SIMO/) SIMONS M.
 XX Edelman ER, Rosenberg RD, Sirols MG, Simons M;
 XX
 DR WPI; 2000-283933/25.
 XX
 PT Antisense inhibition of platelet derived growth factor beta-receptor
 PT subunit expression for the prevention of restenosis -
 XX
 XX Claim 25; Page 15; 43pp; English.
 XX
 CC A method has been developed for preventing restenosis following vascular
 CC injury by antisense inhibition of platelet derived growth factor
 CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
 CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
 CC canal), especially of a valve in the heart, after surgical correction of
 CC the primary condition) following cardiovascular injury. The present
 CC sequence represents a phosphorothioate antisense oligonucleotide for
 CC murine PDGFR-beta.
 XX
 SQ Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 other;

 Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. NO. 2.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 tctgagcactaaagctgg 18
 |||||
 Db 1 tctgagcactaaagctgg 18

 RESULT 2
 AAZ89251
 ID AAZ89251 standard; DNA; 19 BP.
 XX
 AC AAZ89251;
 XX
 DT 09-JUN-2000 (first entry)
 XX
 DE Rat adenosine receptor 2a forward PCR primer.
 XX
 DE Rat; expression profile; Three Prime End Amplification; TPEA;
 KW adenosine receptor 2a; PCR primer; ss.
 XX
 OS Rattus sp.
 XX
 FN WO200008208-A2.
 XX
 PD 17-FEB-2000.
 XX
 XX 05-AUG-1999; 99WO-GB02579.
 PF
 XX 05-AUG-1998; 98GB-0017055.
 PR
 XX (MEDI-) MEDICAL RES COUNCIL.
 PA
 XX Freeman TC, Richardson PJ, Dixon AK;
 PI
 XX WPI; 2000-224033/19.
 DR
 XX
 XX Reverse transcription of mRNA species used for expression profiling of
 PT single cells by employing a first heeled primer to provide first strand
 PT cDNA species and then a second heeled primer population to generate
 PT second strand cDNAs -
 XX
 XX Example 1; Page 30; 50pp; English.
 PS
 XX This invention describes a novel process (M1) of reverse transcribing
 CC mRNA species present in a sample from an organism by: (a) reverse
 CC transcribing the mRNA species using a first heeled primer, to provide a
 CC first strand cDNA species; and (b) synthesizing second cDNA species
 CC using a second heeled primer population, the nucleotide sequences of the

CC non-heel portions of the second heeled primers being such that the
 CC reverse transcribed first strand cDNA species are capable of hybridizing
 CC to at least one second primer. The processes can be used for expression
 CC profiling of single cells. The polynucleotide comprising an oligo d(T)
 CC sequence and a heel sequence 5' can be used for the reverse
 CC transcription of mRNA species in a sample. The polynucleotide primer
 CC population of claim (4) can be used for the synthesis of second strand
 CC cDNA from a population of first strand cDNA species. Single cell cDNA
 CC libraries can be made for subsequent detailed analysis of gene expression
 CC and the discovery of novel genes. Small samples can be used and allow
 CC the utilization of the large amount of sequence data available for
 CC further understanding of disease processes and the cellular physiology of
 CC complex issues. The invention provides a rapid, robust and reproducible
 CC procedure called Three Prime End Amplification (TPEA), optionally with
 CC PCR (TPEA-PCR). Prior art methods for the analysis of gene expression
 CC within single cells or small tissue samples are limiting. Whilst in situ
 CC hybridization techniques provide detailed information about the
 CC cellular expression pattern of a gene in intact tissue the technique is
 CC laborious and unable to analyze multiple transcripts in a single
 CC preparation. The methods presented in the disclosure provide a more
 CC straightforward, reproducible and reliable cDNA amplification procedure
 CC for small mRNA samples where expression profiling can be conducted. The
 CC amplification technique can be carried out in a single tube with a need
 CC for only limited manual intervention and large numbers of samples can
 CC be analyzed. There is a bias towards more uniform length cDNA molecules
 CC ensuring that even relatively low abundance mRNA species are transcribed
 CC and optionally amplified at the same level of efficiency as more
 CC abundant mRNA species. AAZ89191-Z89253 represent the primers described in
 CC the method of the invention.
 XX
 SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 other;

Query Match 73.3%; Score 13.2; DB 21; Length 19;
 Best Local Similarity 83.3%; Pred. NO. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 1 tctgagcactaaagctgg 18
 |||||
 Db 1 tctgaccacaacagctgg 18

 RESULT 3
 AAF57945
 ID AAF57945 standard; DNA; 19 BP.
 XX
 AC AAF57945;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Low abundance nucleic acid amplification PCR primer #16.
 XX
 XX Nucleic acid amplification; low abundance sequence; expression profiling;
 KW high throughput analysis; PCR primer; ss.
 KW
 XX Synthetic.
 OS
 XX WO200106004-A2.
 PN
 XX 25-JAN-2001.
 PD
 XX 19-JUL-2000; 2000WO-EP06887.
 PF
 XX 19-JUL-1999; 99US-0144666.
 PR
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES.
 PA
 XX Richardson P, Cox P;
 PI
 XX WPI; 2001-138470/14.
 DR
 XX Increasing the number of nucleotide sequences for low quantity mRNA
 XX species from a sample for detection and cloning of gene sequences -
 PT

XX PS Example 1; Page 110; 120pp; English.

CC CC The present invention describes methods of increasing the number of

CC CC nucleic acid sequences corresponding to an mRNA present in a sample using

CC CC heeled primer sequences in amplification reactions. This is useful in the

CC CC detection and cloning of low copy number mRNAs in a sample, in expression

CC CC profiling and in high throughput systems.

XX SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 other;

Query Match 73.3%; Score 13.2; DB 22; Length 19;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18

Db 1 tctgaccacaaagctgg 18

RESULT 4

AAZ74041

ID AAZ74041 standard; DNA; 21 BP.

XX AC AAZ74041;

XX DT 10-SEP-2001 (first entry)

XX DE Human biallelic marker downstream amplification primer SEQ ID NO:8397.

XX KW Human genome; biallelic marker; high density disequilibrium map;

XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX KW haplotyping; hybridisation; identification; characterisation;

XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;

XX KW diagnosis; ss.

XX OS Homo sapiens.

XX PN WO9954500-A2.

XX PD 28-OCT-1999.

XX PF 21-APR-1999; 99WO-IB00822.

XX PR 21-APR-1998; 98US-0082614.

XX PR 23-NOV-1998; 98US-0109732.

XX PA (BEST) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I;

XX DR WPI; 2000-013267/01.

XX PT Novel biallelic markers used to construct a high density disequilibrium

XX PT map of the human genome

XX PS Claim 8; Page 2021; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC CC invention, which contain a polymorphic base at position 24 of their

CC CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC CC primers for the biallelic markers. The biallelic markers of the

CC CC invention have a variety of uses: they can be used for high density

CC CC mapping of the human genome, and in complex association studies and

CC CC haplotyping studies which are useful in determining the genetic basis

CC CC for disease states. Compositions and methods of the invention can also

CC CC be useful for the identification of the targets for the development of

CC CC pharmaceutical agents and diagnostic methods, as well as the

CC CC characterisation of the differential efficacious responses to and side

CC CC effects from pharmaceutical agents acting on a disease as well as other

CC CC treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297

CC and 3367, are not actually given a sequence in the Sequence Listing

CC from the present invention.

XX SQ Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 other;

Query Match 73.3%; Score 13.2; DB 21; Length 21;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18

Db 2 tatgagcaccacaaagctgg 19

RESULT 5

AAI61828

ID AAI61828 standard; DNA; 24 BP.

XX AC AAI61828;

XX DT 16-OCT-2001 (first entry)

XX DE Soybean 240017 region G3 DNA forward primer, SEQ ID NO: 459.

XX KW Soybean; antihelminthic; gene therapy; soybean cyst nematode; SCN;

XX KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;

XX KW 240017 region G3; 318013 region A3; 515002 region G2; PCR primer; ss.

XX OS Glycine max.

XX PN WO200151627-A2.

XX PD 19-JUL-2001.

XX PF 05-JAN-2001; 2001WO-US00552.

XX PR 07-JAN-2000; 2000US-0174880.

XX PA (MONS) MONSANTO CO.

XX PI Hauge BM, Wang ML, Parsons JD, Parnell LD;

XX DR WPI; 2001-425872/45.

XX PT New purified nucleic acid for producing a soybean plant having soybean

XX PT cyst nematode resistance and for use in plant breeding programs -

XX PS Claim 25; Page 1149; 1353pp; English.

XX CC The invention relates to nucleic acid molecules from regions of the

CC CC soybean genome which are associated with soybean cyst nematode (SCN)

CC CC resistance. The nucleic acids are used to transform plants, and can

CC CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.

CC CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes

CC CC of soybean plants and for introgressing SCN resistance or partial SCN

CC CC resistance into soybean plants. They can also be used in plant breeding

CC CC programmes. The invention also relates to proteins encoded by such

CC CC nucleic acid molecules, as well as antibodies capable of recognising

CC CC these proteins. The present sequence is a primer used to amplify a

XX CC region of the soybean genome.

XX SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 other;

Query Match 73.3%; Score 13.2; DB 22; Length 24;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18

Db 2 tatgagcaccacaaagctgg 19

```
RESULT 6
AAI61830
ID AAI61830 standard; DNA; 24 BP.
XX
XX AAI61830;
XX
XX 16-OCT-2001 (first entry)
XX
XX Soybean 240017 region G3 DNA forward primer, SEQ ID NO: 461.
XX
XX Soybean; antihelminthic; gene therapy; soybean cyst nematode; SCN;
KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;
KW 240017 region G3; 318013 region A3; 515002 region G2; PCR primer; ss.
XX
XX Glycine max.
OS
XX WO200151627-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-US00552.
XX
XX 07-JAN-2000; 2000US-0174880.
XX
XX (MONS ) MONSANTO CO.
XX
XX Hauge BM, Wang ML, Parsons JD, Parnell LD;
PI
XX WPI; 2001-425872/45.
XX
XX New purified nucleic acid for producing a soybean plant having soybean
PT cyst nematode resistance and for use in plant breeding programs .
XX
XX Claim 25; Page 1149; 1353pp; English.
XX
XX The invention relates to nucleic acid molecules from regions of the
CC soybean genome which are associated with soybean cyst nematode (SCN)
CC resistance. The nucleic acids are used to transform plants, and can
CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.
CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes
CC of soybean plants and for introgressing SCN resistance or partial SCN
CC resistance into soybean plants. They can also be used in plant breeding
CC programmes. The invention also relates to proteins encoded by such
CC nucleic acid molecules, as well as antibodies capable of recognising
CC these proteins. The present sequence is a primer used to amplify a
CC region of the soybean genome.
XX
XX Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 other;
SQ
Query Match 73.3%; Score 13.2; DB 22; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 tctgagcactaaagctgg 18
Db 2 tatgaaccctaaagctgg 19
RESULT 7
AAZ48359/c
ID AAZ48359 standard; DNA; 41 BP.
XX
XX AAZ48359;
XX
XX 27-MAR-2000 (first entry)
XX
XX Primer specific for Giardia sp giardin.
XX
XX Microorganism: virus; polymerase chain reaction; food; cosmetic;
KW clinical diagnostic; molecular beacon; PCR primer; ss.
XX
```

```
OS Giardia sp.
XX WO9963112-A2.
XX
XX 09-DEC-1999.
XX
XX 18-MAY-1999; 99WO-US10940.
XX
XX 18-MAY-1998; 98US-0086025.
XX
XX 17-MAY-1999; 99US-0086025.
XX
XX (HUNT-) HUNT WESSON INC.
XX
XX Romick TL, Fraser MS;
XX
XX WPI; 2000-086985/07.
XX
XX Detection of microorganisms and viruses, for use in the food and
PT cosmetic industries and for clinical diagnostics .
XX
XX Disclosure; Page 19; 63pp; English.
XX
XX The invention provides a novel in vitro method for the detection of
CC microorganisms and viruses. The method comprises: (1) forming a
CC polymerase chain reaction (PCR) mixture by combining a predetermined
CC volume of a sample to be tested for the presence of a nucleic acid
CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer
CC comprising 5'-GCTAAGGTCCTCAAGT-3', and a second primer comprising
CC 5'-AGACGCTCTCTACC-3', and PCR reagents; (2) forming a PCR product by
CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
CC to replicate and attain 0.25-1000mug nucleotide product/mul mixture; (3)
CC adding a probe containing DNA comprising 5'-GGTGGCTGCTTCTAAGCACAC-3', to
CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
CC the nucleic acid sequence, if present, and change the conformation of the
CC probe; and (4) determining whether or not bacteria are present in the
CC sample by detecting the conformational change of the probe, a
CC conformational change indicating the presence of bacteria in the sample.
CC The methods can be used for the detection of viruses and microorganisms,
CC including bacteria, yeast, molds and protista. They can be used in the
CC food and cosmetic industry and in clinical diagnostics. Using the method
CC it is not necessary to remove non-hybridized probe from the system.
XX
XX Sequence 41 BP; 10 A; 9 C; 11 G; 11 T; 0 other;
SQ
Query Match 72.2%; Score 13; DB 21; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 agcactaaagctg 17
Db 28 AGCACTAAGACTG 16
RESULT 8
AAT03932/c
ID AAT03932 standard; DNA; 47 BP.
XX
XX AAT03932;
XX
XX 20-DEC-1995 (first entry)
XX
XX Factor-V NASBA primer P1.
XX
XX Factor-V; thrombosis; thrombophilia; diagnosis; anticoagulant;
KW activated protein-C; APC; homozygosity; heterozygosity;
KW primer; nucleic acid sequence based amplification; NASBA; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..27
FT /*tag= a
```



```

FT XX /function= T7 RNAP promoter sequence
PN XX W09521938-A1.
XX XX
PD XX 17-AUG-1995.
XX XX
PF XX 14-FEB-1995; 95WO-EP00553.
XX XX
PR XX 14-FEB-1994; 94EP-0200377.
XX XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX XX
PI Bertina RM, Reitsma PH;
XX XX
DR WPI; 1995-293134/38.
XX XX
XX Screening for genetic defect associated with thrombosis and/or poor
PT anticoagulant response to activated protein C - useful to determine
PT homozygosity or heterozygosity for a mutation in Factor V, Va, VIII
PT or VIIa.
XX XX
PS Example 3; Page 46; 98pp; English.
XX XX
CC The amplification primers and detection probes given in AAT03932-38
CC are used for NASBA of human Factor-V DNA in order to detect a
CC mutation at codon 506 associated with an increased risk of
CC thrombotic events. Primer P1 is located in exon 10 of the
CC Factor V coding sequence.
XX XX
SQ Sequence 47 BP; 13 A; 10 C; 8 G; 16 T; 0 other;

Query Match 71.1%; Score 12.8; DB 16; Length 47;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tgagcactaaagctgg 18
Db 47 TGAGAACAAAAGCTGG 32

RESULT 9
AAZ74877
ID AAZ74877 standard; DNA; 18 BP.
AC AAZ74877;
XX XX
DT 10-SEP-2001 (first entry)
DE Human biallelic marker downstream amplification primer SEQ ID NO:9233.
XX XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX XX
OS Homo sapiens.
XX XX
PN W09954500-A2.
XX XX
PD 28-OCT-1999.
XX XX
PF 21-APR-1999; 99WO-IB00822.
XX XX
PR 21-APR-1998; 98US-0082614.
XX XX
PR 23-NOV-1998; 98US-0109732.
XX XX
PA (GEST ) GENSET.
XX XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX XX
DR WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX XX
PS Claim 8; Page 2199; 2745pp; English.
XX XX
AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX XX
SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 other;

Query Match 68.9%; Score 12.4; DB 21; Length 18;
Best Local Similarity 92.9%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 agcactaaagctgg 18
Db 2 agcactgaagctgg 15

RESULT 10
AAH38346/C
ID AAH38346 standard; DNA; 27 BP.
XX XX
AC AAH38346;
XX XX
DT 14-AUG-2001 (first entry)
DE SNP specific lower PCR primer SEQ ID 1142.
XX XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX XX
OS Homo sapiens.
XX XX
PN WO200129262-A2.
XX XX
PD 26-APR-2001.
XX XX
PF 13-OCT-2000; 2000WO-US28436.
XX XX
PR 15-OCT-1999; 99US-0160096.
XX XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX XX
PI Picoult-Newburg L, Pohl M;
XX XX
DR WPI; 2001-290930/30.
XX XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample -
XX XX
PS Claim 1; Page 55; 83pp; English.

```

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence.

XX
SQ Sequence 27 BP; 9 A; 5 C; 6 G; 7 T; 0 other;

Query Match 68.9%; Score 12.4; DB 22; Length 27;
Best Local Similarity 92.9%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1 tctgagcactaaag 14
||||| |||||

DB 26 TCTGACACTAAG 13

RESULT 11

AAH72197
ID AAX72197 standard; RNA; 27 BP.
XX
AC AAX72197;
XX
XX 28-JUL-1999 (first entry)
DE
DE Mouse flk-1 VEGF receptor hammerhead ribozyme #441.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Synthetic.
OS Mus sp.
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US17480.
PF
XX
XX 11-JAN-1996; 96US-0584040.
PR
XX 26-OCT-1995; 95US-0005974.
PR
XX
XX (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
PI WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or

PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 9; Page 136; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.

XX Sequence 27 BP; 9 A; 6 C; 7 G; 4 U; 1 other;

Query Match 67.8%; Score 12.2; DB 18; Length 27;
Best Local Similarity 61.1%; Pred. No. 3.9e+03;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
:|:| | |||||

DB 8 ucugaugangaaagcugg 25

RESULT 12

AAZ12424/C
ID AAZ12424 standard; DNA; 30 BP.
XX
AC AAZ12424;
XX
DT 08-OCT-1999 (first entry)
XX
DE PCR primer used to amplify ORF35 of *Neisseria* species.
XX
KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;
KW treatment; *Neisseria* infection; meningitis; septicaemia; gonorrhea;
KW PCR primer; ss.
XX
OS Synthetic.
OS *Neisseria* sp.
XX
PN WO9924578-A2.
XX
XX 20-MAY-1999.
PD
XX
XX 09-OCT-1998; 98WO-IB01665.
PF
XX
XX 01-SEP-1998; 98GB-0019016.
PR
XX 06-NOV-1997; 97GB-0023516.
PR
XX 14-NOV-1997; 97GB-0024190.
PR
XX 18-NOV-1997; 97GB-0024386.
PR
XX 27-NOV-1997; 97GB-0025158.
PR
XX 10-DEC-1997; 97GB-0026147.
PR
XX 14-JAN-1998; 98GB-0000759.
XX
XX (CHIR-) CHIRON SPA.
PA
XX
XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
PI WPI; 1999-327407/27.
XX
XX Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for
PT diagnosis, treatment and prevention of infection
PT
XX
XX Disclosure; Page 489; 524pp; English.
PS
XX
XX PCR primers AAZ12359-Z12531 were used to amplify various open reading
CC frames (ORFs) of *Neisseria meningitidis* and *N. gonorrhoeae*. These
CC ORFs (AAZ11972-Z12358) encode antigenic proteins (AAZ38499-Y38944). The

CC antigenic proteins, their fragments, their nucleic acids and antibodies
 CC are used for diagnosis, prevention (as vaccines) or treatment of
 CC *Neisseria* infections, such as meningitis, septicemia and gonorrhea.
 CC Both organisms are closely related. Fragments of the nucleic acids are
 CC useful as hybridisation probes and antisense reagents.

XX Sequence 30 BP; 5 A; 10 C; 8 G; 7 T; 0 other;
 SQ

Query Match 67.8%; Score 12.2; DB 20; Length 30;
 Best Local Similarity 82.4%; Pred. No. 3.9e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ctgagcactaaagctgg 18
 ||||| || |||||
 Db 27 CTGAGCTCTGAAGCTAG 11

RESULT 13
 AAZ55464/C
 ID AAZ55464 standard; DNA; 30 BP.

XX AAZ55464;

XX 21-MAR-2000 (first entry)

XX *Neisseria* species ORF cloning PCR primer #849.

XX *Neisseria* meningitidis; *Neisseria* gonorrhea; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
 KW antibacterial; gene therapy; PCR primer; ss.

XX Synthetic.

OS *Neisseria* sp.

XX WO9957280-A2.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US09346.

XX 01-MAY-1998; 98US-0083758.

XX 31-JUL-1998; 98US-0094869.

XX 02-SEP-1998; 98US-0098994.

XX 02-SEP-1998; 98US-0099062.

XX 09-OCT-1998; 98US-0103749.

XX 09-OCT-1998; 98US-0103794.

XX 09-OCT-1998; 98US-0103796.

XX 25-FEB-1999; 99US-0121528.

XX (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

XX Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
 PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
 PI Tettelin H, Venter JC;

XX WPI; 2000-062150/05.

XX Novel *Neisseria* polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics -

XX Example 16; Page 164; 1453pp; English.

XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAZ74253 to AAZ75941
 CC represent novel *Neisseria* meningitis and *N. gonorrhea* polynucleotides
 CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC *Neisseria* bacteria (e.g. meningitis and septicaemia), to detect the

CC presence of *Neisseria* bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.

XX Sequence 30 BP; 5 A; 10 C; 8 G; 7 T; 0 other;

Query Match 67.8%; Score 12.2; DB 21; Length 30;
 Best Local Similarity 82.4%; Pred. No. 3.9e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ctgagcactaaagctgg 18
 ||||| || |||||
 Db 27 CTGAGCTCTGAAGCTAG 11

RESULT 14
 AAQ92440
 ID AAQ92440 standard; DNA; 38 BP.

XX AAQ92440;

XX 11-JAN-1996 (first entry)

XX TCR gamma constant region 5' PCR detection primer.

XX Primer; PCR; amplification; natural killer cell; purification; CD3; CD5;
 KW antibody; interleukin; proliferation; target cell type; beta-actin;
 KW allogenic lymphoblastoid; T-cell receptor; gene expression; ss.

XX Synthetic.

XX US5415874-A.

XX 16-MAY-1995.

XX 31-OCT-1989; 89US-0429353.

XX 31-OCT-1989; 89US-0429353.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Bender JR, Engleman EG, Pardi R;

XX WPI; 1995-193394/25.

XX Prodn. of target cell-specific natural killer cells - by selecting
 PT natural killer cells based on their adhesion to a selected target
 PT cell type and culturing.

XX Example 5; Column 15; 23pp; English.

XX Primers AAQ92434-49 were used to PCR detect specific messenger RNAs in
 CC cultured natural killer (NK) cells. The NK cells are purified by
 CC partial purification through a nylon wool column followed by removal
 CC of the CD3+ and CD5+ cells by incubating in the presence of bound
 CC anti-CD3 and anti-CD5 antibodies. The remaining cells which express
 CC the Leu16+ (CD16) and Leu19 markers are enriched by propagating in a
 CC medium containing an agent e.g. interleukin (IL)-2 which promotes
 CC proliferation of the NK cells and in the presence of the NK cells,
 CC target cell type e.g. allogenic lymphoblastoid cells.

XX Confirmation of the correct NK cell type is carried by PCR amplification
 CC of the CD3 and T-cell receptor (TCR) markers alpha, beta, gamma and
 CC delta, on reverse transcribed RNA isolated from the NK cells. The
 CC primers AAQ92440-1 target the T-cell receptor gene gamma constant
 CC region.

XX Sequence 38 BP; 12 A; 9 C; 8 G; 9 T; 0 other;

Query Match 67.8%; Score 12.2; DB 16; Length 38;
 Best Local Similarity 82.4%; Pred. No. 4e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctg 17
 ||||| 1 1
Db 7 tctgagcactagattg 23

RESULT 15
AAH43130/C
ID AAH43130 standard; cDNA; 39 BP.
XX
AC AAH43130;
XX
DT 17-OCT-2001 (first entry)
XX
DE Primer: F5-alpha-top.
XX
KW T cell receptor; TCR; influenza A; ligand; functional processing;
KW affinity; polymerase chain reaction; primer; amplify; PCR; ss.
XX
OS Synthetic.
XX
PN EP1118661-Al.
XX
PD 25-JUL-2001.
XX
PF 13-JAN-2000; 2000EP-0200110.
XX
PR 13-JAN-2000; 2000EP-0200110.
XX
PA (HETN-) HET NEDERLANDS KANKER INST.
XX
PI Schumacher ANM, Kessels HWHG;
XX
DR WPI; 2001-459002/50.
XX

CC The sequences given in AAH43128-34 are primers which were used in the
CC amplification and cloning of the complementarity determining regions
CC (CDR3) of a T cell receptor which was generated by the method of the
CC invention. The method of the invention allows generation of receptors
CC with desired specificities for ligands, which upon binding to the
CC ligand under-go functional processing in order to provide a biological
CC response after ligand-binding. The method is used for generating
CC libraries of cells with receptors of differing affinities.
XX
SQ Sequence 39 BP; 10 A; 9 C; 9 G; 11 T; 0 other;

Query Match 66.7%; Score 12; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 cactaaagctgg 18
 |||||
Db 39 CACTAAAGCTGG 28

Search completed: October 12, 2002, 17:08:01
Job time: 9746 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:34 ; Search time 191.26 Seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18

Sequence: 1 tctgacactaaagctgg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.2	67.8	27	4	US-08-584-040-4947
2	11.8	65.6	28	4	US-09-129-686-14
3	11.8	65.6	34	4	US-08-532-657A-11
4	11.6	64.4	30	1	US-08-321-613-9
5	11.6	64.4	38	3	US-08-850-961-3
6	11.6	64.4	38	4	US-09-479-776-3
7	11.4	63.3	22	1	US-08-609-572-9
8	11.4	63.3	22	4	US-08-841-751-9
9	11.4	63.3	22	4	US-08-846-344-9
10	11.4	63.3	22	4	US-08-846-344-9
11	11.4	63.3	25	3	US-08-343-998-12
12	11.2	62.2	21	1	US-07-922-723A-30
13	11.2	62.2	21	1	US-07-799-828C-30
14	11.2	62.2	21	2	US-07-952-277A-30
15	11.2	62.2	25	3	US-09-132-541-10
16	11.2	62.2	27	1	US-08-758-306-164
17	11.2	62.2	27	1	US-08-758-306-708
18	11.2	62.2	27	1	US-08-758-306-720
19	11.2	62.2	27	1	US-08-758-306-746
20	11.2	62.2	27	1	US-08-758-306-1116
21	11.2	62.2	27	1	US-08-758-306-1136
22	11.2	62.2	27	2	US-08-956-242-12
23	11.2	62.2	27	3	US-08-985-162-1115
24	11.2	62.2	27	3	US-08-985-162-1220
25	11.2	62.2	27	3	US-09-351-215-12
26	11.2	62.2	27	3	US-08-998-099-144
27	11.2	62.2	27	3	US-08-998-099-220

28 11.2 62.2 27 3 US-08-998-099-280
29 11.2 62.2 27 4 US-08-584-040-82
30 11.2 62.2 27 4 US-08-584-040-806
31 11.2 62.2 27 4 US-08-584-040-3177
32 11.2 62.2 27 4 US-08-584-040-3392
33 11.2 62.2 27 4 US-08-584-040-3524
34 11.2 62.2 27 4 US-08-584-040-3713
35 11.2 62.2 27 4 US-08-584-040-3735
36 11.2 62.2 27 4 US-08-584-040-4714
37 11.2 62.2 27 4 US-08-584-040-4822
38 11.2 62.2 27 4 US-08-584-040-5106
39 11.2 62.2 27 4 US-08-584-040-6345
40 11.2 62.2 27 4 US-08-584-040-6683
41 11.2 62.2 27 4 US-08-584-040-6685
42 11.2 62.2 27 4 US-08-584-040-6866
43 11.2 62.2 27 4 US-08-584-040-6827
44 11.2 62.2 27 4 US-08-584-040-7036
45 11.2 62.2 27 4 US-08-584-040-7080

ALIGNMENTS

RESULT 1
US-08-584-040-4947
; Sequence 4947, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4947:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Sequence 280, Ap
Sequence 82, Appl
Sequence 806, Ap
Sequence 3177, Ap
Sequence 3392, Ap
Sequence 3524, Ap
Sequence 3713, Ap
Sequence 3735, Ap
Sequence 4714, Ap
Sequence 4822, Ap
Sequence 5106, Ap
Sequence 6345, Ap
Sequence 6683, Ap
Sequence 6685, Ap
Sequence 6827, Ap
Sequence 7036, Ap
Sequence 7080, Ap

```
;
; FEATURE:
; OTHER INFORMATION: The letter "N" represents the stem II region
; OTHER INFORMATION: of an HH ribozyme.
; US-08-584-040-4947

Query Match          67.8%; Score 12.2; DB 4; Length 27;
Best Local Similarity 61.1%; Pred. No. 2.9e+02;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
      :||| | |||||:|
Db 8 UCUGAUGAAGAACUGG 25

RESULT 2
US-09-129-686-14
; Sequence 14, Application US/09129686A
; Patent No. 6264940
; GENERAL INFORMATION:
; APPLICANT: Gromeier PhD, Matthias
; APPLICANT: Wimmer Prof, Eckard
; TITLE OF INVENTION: Recombinant Poliovirus For The Treatment of Cancer
; FILE REFERENCE: Recomb Poliovirus for Cancer Treatment
; CURRENT APPLICATION NUMBER: US/09/129,686A
; CURRENT FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Poliovirus Type 1 Mahoney
; US-09-129-686-14

Query Match          65.6%; Score 11.8; DB 4; Length 28;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16
      | ||||| |||||
Db 3 cggagcaataaagct 17

RESULT 3
US-08-532-657A-11/c
; Sequence 11, Application US/08532657A
; Patent No. 6346414
; GENERAL INFORMATION:
; APPLICANT: JACOBS, Eric
; TITLE OF INVENTION: TRANSPORTATION ASSEMBLY FOR GENE TRANSFER
; TITLE OF INVENTION: IN EUKARYOTES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,657A
; FILING DATE: 16-OCT-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: WO PCT/FR94/00419
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
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;
; APPLICATION NUMBER: FR 93/04530
; FILING DATE: 16-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 017753-069
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: synthetic oligonucleotide
; US-08-532-657A-11

Query Match          65.6%; Score 11.8; DB 4; Length 34;
Best Local Similarity 86.7%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16
      | ||||| |||||
Db 21 CAGAGCAGCTGAAGCT 7

RESULT 4
US-08-321-613-9
; Sequence 9, Application US/08321613
; Patent No. 5789247
; GENERAL INFORMATION:
; APPLICANT: BALLAY, ANNICK
; APPLICANT: BOFFA, GEORGES
; APPLICANT: CARTRON, JEAN-PIERRE
; APPLICANT: CHRETEIN, STANY
; APPLICANT: LAMBIN, PATRICK
; APPLICANT: LOPEZ, CLAUDE
; APPLICANT: SALMON, CHARLES
; TITLE OF INVENTION: EXPRESSION IN NON-TUMORAL HUMAN
; TITLE OF INVENTION: LYMPHOBLASTOID LINES WITH AN INTEGRATIVE VECTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,613
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1217-130
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-321-613-9

Query Match 64.4%; Score 11.6; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
||| ||||| ||| ||
Db 5 TCTAGCACTTGAGCAGG 22

RESULT 5
US-08-850-961-3
; Sequence 3, Application US/08850961
; Patent No. 6013517
; GENERAL INFORMATION:
; APPLICANT: Respass, James G.
; APPLICANT: De Polo, Nicholas J.
; APPLICANT: Chada, Sunil
; APPLICANT: Sauter, Sybille
; APPLICANT: Bodner, Mordechai
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: CROSSLESS RETROVIRAL VECTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation, Intellectual Property - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850.961
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kruse, No. 6013517/man J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 930049.424C4 / 1147.005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-3520
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 64.4%; Score 11.6; DB 3; Length 38;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
||| ||||| ||| ||
Db 10 TCTGAGATTAAGGCTAG 27

RESULT 6
US-09-479-776-3
; Sequence 3, Application US/09479776

; Patent No. 6333195
; GENERAL INFORMATION:
; APPLICANT: Respass, James G.
; APPLICANT: De Polo, Nicholas J.
; APPLICANT: Chada, Sunil
; APPLICANT: Sauter, Sybille
; APPLICANT: Bodner, Mordechai
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: CROSSLESS RETROVIRAL VECTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY-R440
; P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,776
; FILING DATE: 07-Jan-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KRUSE, NORMAN J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 930049.424C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)622-4900
; TELEFAX: (206)682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-479-776-3

Query Match 64.4%; Score 11.6; DB 4; Length 38;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
||| ||||| ||| ||
Db 10 TCTGAGATTAAGGCTAG 27

RESULT 7
US-08-609-572-9
; Sequence 9, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; US-08-609-572-9

Query Match 63.3%; Score 11.4; DB 1; Length 22;
Best Local Similarity 92.3%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctgagcactaaa 13
|||||
DB 3 TCTGAGCAATAAA 15

RESULT 8
US-08-841-751-9
; Sequence 9, Application us/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; US-08-841-751-9

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctgagcactaaa 13
|||||
DB 3 TCTGAGCAATAAA 15

RESULT 9
US-08-846-340-9
; Sequence 9, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; US-08-846-340-9

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```
Qy 1 tctgagcactaaa 13
    ||||| ||||
Db 3 TCTGAGCAATAAA 15

RESULT 10
US-08-846-344-9
; Sequence 9, Application US/08846344
; Patent No. 6268480
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
US-08-846-344-9

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctgagcactaaa 13
    ||||| ||||
Db 3 TCTGAGCAATAAA 15

RESULT 11
US-08-343-998-12
; Sequence 12, Application US/08343998A
; Patent No. 6020123
; GENERAL INFORMATION:
; APPLICANT: Sonigo, Pierre
; APPLICANT: Brechot, Christian
; APPLICANT: Courgnard, Valerie
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES FOR THE AMPLIFICATION OF THE
; TITLE OF INVENTION: GENOME OF THE RETROVIRUSES OF THE HIV-2 AND SIV TYPE,
```

```

; TITLE OF INVENTION: AND THEIR USES FOR IN VITRO DIAGNOSIS OF THE INFECTIONS
; TITLE OF INVENTION: DUE TO THESE VIRUSES
; FILE REFERENCE: 2356.0065-01
; CURRENT APPLICATION NUMBER: US/08/343,998A
; CURRENT FILING DATE: 1994-11-18
; EARLIER APPLICATION NUMBER: 07/920,600
; EARLIER FILING DATE: 1992-01-22
; EARLIER APPLICATION NUMBER: PCT/FR90/00394
; EARLIER FILING DATE: 1990-06-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 2
; FEATURE:
US-08-343-998-12

Query Match 63.3%; Score 11.4; DB 3; Length 25;
Best Local Similarity 92.3%; Pred. No. 8.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ctgagcactaaaag 14
    ||| ||||| ||||
Db 12 ctgtgcactaaaag 24

RESULT 12
US-07-922-723A-30/c
; Sequence 30, Application US/07922723A
; Patent No. 5369004
; GENERAL INFORMATION:
; APPLICANT: Drs. Mihael H. Polymeropoulous
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, Leblanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/922,723A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34506
; REFERENCE/DOCKET NUMBER: 717081B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-922-723A-30

Query Match 62.2%; Score 11.2; DB 1; Length 21;
Best Local Similarity 81.2%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 tgagcactaaagctgg 18
|| ||||| |||||
Db 21 TGCACACTAAGGCTGG 6

RESULT 13
US-07-799-828C-30/c
; Sequence 30, Application US/07799828C
; Patent No. 5378602
; GENERAL INFORMATION:
; APPLICANT: Drs. Carl R. Merrill and
; APPLICANT: Michael H. Polymeropoulos
; TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE
; TITLE OF INVENTION: MICROSTATELLITE REPEAT
; TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; FILING DATE: 19911127
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 717081A
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-799-828C-30

Query Match 62.2%; Score 11.2; DB 1; Length 21;
Best Local Similarity 81.2%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgagcactaaagctgg 18
|| ||||| |||||
Db 21 TGCACACTAAGGCTGG 6

RESULT 14
US-07-952-277A-30/c
; Sequence 30, Application US/07952277A
; Patent No. 5861504
; GENERAL INFORMATION:
; APPLICANT: Drs. Michael H. Polymeropoulos
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: ELEVEN HIGHLY INFORMATIVE
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
```

```
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/952,277A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34506
; REFERENCE/DOCKET NUMBER: 717081C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-952-277A-30
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Query Match 62.2%; Score 11.2; DB 2; Length 21;
Best Local Similarity 81.2%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgagcactaaagctgg 18
|| ||||| |||||
Db 21 TGCACACTAAGGCTGG 6
```

```
RESULT 15
US-09-132-541-10/c
; Sequence 10, Application US/09132541A
; Patent No. 6114113
; GENERAL INFORMATION:
; APPLICANT: MCLAUGHLIN-TAYLOR, Elizabeth
; APPLICANT: KRUGER, Mark
; APPLICANT: LUNDAK, Cheryl
; APPLICANT: KILLION, Catherine
; TITLE OF INVENTION: HIGH EFFICIENCY GENETIC MODIFICATION METHODS
; FILE REFERENCE: 1386.002
; CURRENT APPLICATION NUMBER: US/09/132,541A
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 60/055,453
; EARLIER FILING DATE: 1997-08-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This information is not availa
US-09-132-541-10
```

```
Query Match 62.2%; Score 11.2; DB 3; Length 25;
Best Local Similarity 81.2%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgagcactaaagctgg 18
|| || ||||| |||||
Db 19 TGAGACCAAAAGCTGG 4
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Search completed: October 12, 2002, 16:54:35

Job time: 8990 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:28 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18

Sequence: 1 tctgagcactaaagctgg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
 - 32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
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- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	18	16	US-09-241-561-2	Sequence 2, Appli
2	14	77.8	25	62	US-60-232-638-45566	Sequence 45566, A
3	13.8	76.7	25	17	US-09-396-196F-84671	Sequence 84671, A
4	13.8	76.7	25	35	US-09-954-427-390832	Sequence 390832, A
5	13.8	76.7	25	62	US-60-233-166-390832	Sequence 390832, A
6	13.4	74.4	25	62	US-60-232-638-99211	Sequence 99211, A
7	13.4	74.4	25	62	US-60-232-638-99219	Sequence 99219, A
8	13.4	74.4	25	74	US-60-353-987-889590	Sequence 889590, A
9	13.4	74.4	25	74	US-60-353-987-918095	Sequence 918095, A
10	13.4	74.4	25	74	US-60-353-987-918095	Sequence 918095, A
11	13.4	74.4	50	1	PCT-US01-47856-2395	Sequence 2395, Ap
12	13.2	73.3	19	16	US-09-288-674-53	Sequence 53, Appli
13	13.2	73.3	21	18	US-09-422-978-8397	Sequence 8397, Ap
14	13.2	73.3	21	74	US-60-350-061-525	Sequence 525, App
15	13.2	73.3	24	29	US-09-754-853A-459	Sequence 459, App
16	13.2	73.3	24	29	US-09-754-853A-461	Sequence 461, App
17	13.2	73.3	25	35	US-09-954-427-410579	Sequence 410579, A
18	13.2	73.3	25	62	US-60-233-166-410579	Sequence 410579, A
19	13.2	73.3	25	62	US-60-234-049-46404	Sequence 46404, A
20	13.2	73.3	25	74	US-60-353-987-281238	Sequence 281238, A
21	13.2	73.3	25	74	US-60-353-987-594497	Sequence 594497, A
22	13.2	73.3	42	74	US-60-353-790-2578	Sequence 2578, Ap
23	13.2	73.3	47	47	US-60-082-614-236	Sequence 236, App
24	13.2	73.3	47	47	US-60-082-614-889	Sequence 889, App
25	13	72.2	25	62	US-60-234-049-88435	Sequence 88435, A
26	13	72.2	31	18	US-09-465-684-1427	Sequence 1427, Ap
27	13	72.2	41	17	US-09-313-221A-44	Sequence 44, Appli
28	12.8	71.1	23	24	US-09-634-306B-176505	Sequence 176505, A
29	12.8	71.1	25	17	US-09-396-196F-53894	Sequence 53894, A
30	12.8	71.1	25	17	US-09-396-196F-69541	Sequence 69541, A
31	12.8	71.1	25	17	US-09-396-196F-84670	Sequence 84670, A

32 12.8 71.1 25 17 US-09-396-196F-105745, Sequence 105745,
c 33 12.8 71.1 25 35 US-09-956-584-491250, Sequence 491250,
c 34 12.8 71.1 25 35 US-09-956-584-491255, Sequence 491255,
35 12.8 71.1 25 62 US-60-232-638-17717, Sequence 17717, A
36 12.8 71.1 25 62 US-60-232-638-65760, Sequence 65760, A
37 12.8 71.1 25 62 US-60-232-638-98702, Sequence 98702, A
38 12.8 71.1 25 62 US-60-232-638-98714, Sequence 98714, A
39 12.8 71.1 25 62 US-60-232-638-107394, Sequence 107394,
40 12.8 71.1 25 62 US-60-232-638-107401, Sequence 107401,
c 41 12.8 71.1 25 62 US-60-234-017-517971, Sequence 517971,
c 42 12.8 71.1 25 62 US-60-234-017-517972, Sequence 517972,
43 12.8 71.1 25 74 US-60-353-987-729035, Sequence 729035,
44 12.8 71.1 47 60 US-60-216-745-3116, Sequence 3116, Ap
45 12.4 68.9 18 18 US-09-422-978-9233, Sequence 9233, Ap

ALIGNMENTS

RESULT 1
US-09-241-561-2
; Sequence 2, Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-2

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
Db 1 tctgagcactaaagctgg 18
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RESULT 2
US-60-232-638-45566
; Sequence 45566, Application US/60232638
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: SGD YDL187C
US-60-232-638-45566

Query Match 77.8%; Score 14; DB 62; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgagcactaaagct 16
Db 11 tgagcactaaagct 24
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RESULT 3
US-09-396-196F-84671/c
; Sequence 84671, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84671
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-84671

Query Match 76.7%; Score 13.8; DB 17; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagctgg 18
Db 20 CTGAGCACTAAATATGG 4
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RESULT 4
US-09-954-427-390832/c
; Sequence 390832, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390832
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-09-954-427-390832

Query Match 76.7%; Score 13.8; DB 35; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagctgg 18
|||||

Db 22 CTGAGACCTAAAGCTGG 6

RESULT 5

US-60-233-166-390832/c

; Sequence 390832, Application US/60233166

; GENERAL INFORMATION:

; APPLICANT: Mitmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat

; FILE REFERENCE: 3112

; CURRENT APPLICATION NUMBER: US/60/233.166

; CURRENT FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 420907

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 390832

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Affymetrix Proprieta

US-60-233-166-390832

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 62; Length 25;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagctgg 18

||||| |||||||||

Db 22 CTGAGACCTAAAGCTGG 6

RESULT 6

US-60-232-638-99211/c

; Sequence 99211, Application US/60232638

; GENERAL INFORMATION:

; APPLICANT: Mitmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast

; FILE REFERENCE: 3110

; CURRENT APPLICATION NUMBER: US/60/232,638

; CURRENT FILING DATE: 2000-09-14

; NUMBER OF SEQ ID NOS: 138410

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 99211

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: SGD YLR196W

US-60-232-638-99211

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 62; Length 25;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16

||||| |||||||||

Db 25 CAGAGCACTAAAGCT 11

RESULT 7

US-60-232-638-99219/c

; Sequence 99219, Application US/60232638

; GENERAL INFORMATION:

; APPLICANT: Mitmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast

; FILE REFERENCE: 3110

; CURRENT APPLICATION NUMBER: US/60/232,638

; CURRENT FILING DATE: 2000-09-14

; NUMBER OF SEQ ID NOS: 138410

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 99219

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: SGD YLR196W

US-60-232-638-99219

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 62; Length 25;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16

||||| |||||||||

Db 19 CAGAGCACTAAAGCT 5

RESULT 8

US-60-353-987-564374/c

; Sequence 564374, Application US/60353987

; GENERAL INFORMATION:

; APPLICANT: Mitmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133

; FILE REFERENCE: 3121

; CURRENT APPLICATION NUMBER: US/60/353,987

; CURRENT FILING DATE: 2002-02-01

; NUMBER OF SEQ ID NOS: 997516

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 564374

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-60-353-987-564374

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 74; Length 25;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16

||||| |||||||||

Db 16 CTGATCACTAAAGCT 2

RESULT 9

US-60-353-987-889590/c

; Sequence 889590, Application US/60353987

; GENERAL INFORMATION:

; APPLICANT: Mitmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133

; FILE REFERENCE: 3121

; CURRENT APPLICATION NUMBER: US/60/353,987

; CURRENT FILING DATE: 2002-02-01

; NUMBER OF SEQ ID NOS: 997516

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 889590

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-60-353-987-889590

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 74; Length 25;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctgagcactaaagc 15

||||| |||||||||

Db 17 TCTGAGTACTAAAGC 3

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RESULT 10
US-60-353-987-918095/c
; Sequence 918095, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 918095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-353-987-918095

Query Match          74.4%; Score 13.4; DB 74; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgagcactaaagctg 17
Db 20 TGAGCACTAAAGGTG 6

RESULT 11
PCT-US01-47856-2395
; Sequence 2395, Application PC/TUS0147856
; GENERAL INFORMATION:
; APPLICANT: BIOCARDIA, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Quertermous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 506612000140
; CURRENT APPLICATION NUMBER: PCT/US01/47856
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2395
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47856-2395

Query Match          74.4%; Score 13.4; DB 1; Length 50;
Best Local Similarity 93.3%; Pred. No. 8.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 gagcactaaagctg 18
Db 17 gagaactaaagctg 31

RESULT 12
US-09-288-674-53
; Sequence 53, Application US/09288674
; GENERAL INFORMATION:
; APPLICANT: Freeman, Thomas C.
; APPLICANT: Richardson, Peter J.
; APPLICANT: Dickson, Alistair K.
; TITLE OF INVENTION: REVERSE TRANSCRIPTION AND AMPLIFICATION PROCESSES AND
; FILE REFERENCE: HLBB-6
; CURRENT APPLICATION NUMBER: US/09/288,674
; CURRENT FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: GB 98/17055.8
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; OTHER INFORMATION: primer
US-09-288-674-53

Query Match          73.3%; Score 13.2; DB 16; Length 19;
Best Local Similarity 83.3%; Pred. No. 9.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctg 18
Db 1 tctgaccacaagaagctgg 18

RESULT 13
US-09-422-978-8397
; Sequence 8397, Application US/09422978
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020Cp1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8397
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-1515 for SEQ 532, in comple
US-09-422-978-8397

Query Match          73.3%; Score 13.2; DB 18; Length 21;
Best Local Similarity 83.3%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctg 18
Db 2 tatgagcaccacaaggtgg 19

RESULT 14
US-60-350-061-525/c
; Sequence 525, Application US/60350061
; GENERAL INFORMATION:
```


; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; FILE REFERENCE: D0185
; CURRENT APPLICATION NUMBER: US/60/350,061
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 525
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-350-061-525

Query Match 73.3%; Score 13.2; DB 74; Length 21;
Best Local Similarity 83.3%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
| | | | | | | | | | | | | | | | | | | | | |
Db 18 TCTGAGCACTCAAGGAGG 1

RESULT 15
US-09-754-853A-459
; Sequence 459, Application US/09754853A
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 459
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 240017_region_G3_137548_13_Forward_Primer
US-09-754-853A-459

Query Match 73.3%; Score 13.2; DB 29; Length 24;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
| | | | | | | | | | | | | | | | | | | | | |
Db 2 tatgaaccctaaagctgg 19

Search completed: October 12, 2002, 20:42:29
Job time: 16399 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:27 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18

Sequence: 1 tctgagcactaaagctgg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-2
c 2	13.8	76.7	25	5	Sequence 2, Appli
3	13.4	74.4	50	6	Sequence 84671, A
4	13.4	74.4	50	6	Sequence 2395, Ap
5	13.2	73.3	19	6	Sequence 2395, Ap
6	13.2	73.3	19	6	Sequence 16, Appl
7	13.2	73.3	25	5	Sequence 12259, A
8	13	72.2	25	5	Sequence 107078, A
c 9	12.8	71.1	23	7	Sequence 176505, A
10	12.8	71.1	25	5	Sequence 53894, A
11	12.8	71.1	25	5	Sequence 69541, A
c 12	12.8	71.1	25	5	Sequence 84670, A
13	12.8	71.1	25	5	Sequence 105745, A
c 14	12.4	68.9	20	1	PCT-US01-44838-533
c 15	12.4	68.9	25	5	Sequence 533, App
16	12.4	68.9	32	1	Sequence 117149, A
17	12.4	68.9	32	1	Sequence 5, Appli
c 18	12.4	68.9	50	6	Sequence 2809, Ap
19	12.2	67.8	25	5	Sequence 84671, A
20	12.2	67.8	25	5	Sequence 141477, A
c 21	12.2	67.8	25	5	Sequence 17263, A
c 22	12.2	67.8	25	5	Sequence 39866, A
23	12.2	67.8	25	5	Sequence 83717, A
24	12.2	67.8	25	5	Sequence 95491, A
c 25	12.2	67.8	25	5	Sequence 118195, A
					Sequence 122369, A

26 12.2 67.8 50 6 US-10-131-831-2599 Sequence 2599, Ap
27 12.2 67.8 50 6 US-10-131-827-2599 Sequence 2599, Ap
c 28 11.8 65.6 21 1 PCT-US01-44838-648 Sequence 3, Appli
c 29 11.8 65.6 24 6 US-10-131-827-8918 Sequence 8918, Ap
c 30 11.8 65.6 25 5 US-09-956-604-16893 Sequence 16893, A
c 31 11.8 65.6 25 5 US-09-396-196G-53893 Sequence 53893, A
c 32 11.8 65.6 25 5 US-09-396-196G-69540 Sequence 69540, A
33 11.8 65.6 25 5 US-09-396-196G-105734 Sequence 105734, A
34 11.8 65.6 25 5 US-09-396-196G-105734 Sequence 8, Appli
35 11.8 65.6 26 6 US-10-131-332A-8 Sequence 14, Appli
36 11.8 65.6 28 7 US-10-175-247-14 Sequence 16, Appli
37 11.8 65.6 36 5 US-09-601-997-16 Sequence 18, Appli
38 11.8 65.6 36 6 US-10-244-715-18 Sequence 20401, A
39 11.8 65.6 37 7 US-10-138-674-20401 Sequence 18, Appli
40 11.8 65.6 38 1 PCT-US02-23214-18 Sequence 18, Appli
41 11.8 65.6 38 6 US-10-197-816-18 Sequence 1761, Ap
42 11.8 65.6 50 6 US-10-131-831-1761 Sequence 1907, Ap
43 11.8 65.6 50 6 US-10-131-827-1761 Sequence 1761, Ap
44 11.8 65.6 50 6 US-10-131-827-1761 Sequence 1907, Ap
45 11.8 65.6 50 6 US-10-131-827-1907 Sequence 1907, Ap

ALIGNMENTS

RESULT 1
US-09-945-131-2
; Sequence 2, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-2

Query Match 100.0% Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred.No. 2.7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18
Db 1 tctgagcactaaagctgg 18

RESULT 2
US-09-396-196G-84671/c
; Sequence 84671, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84671
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-84671

Query Match 76.7%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ctgagcactaaagctgg 18
||| ||||| |||
Db 20 CTGAGCACTAAATATGG 4

RESULT 3
US-10-131-831-2395
; Sequence 2395, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2395
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-2395

Query Match 74.4%; Score 13.4; DB 6; Length 50;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 gagcactaaagctgg 18
||| ||||| |||
Db 17 gagaactaaagctgg 31

RESULT 4
US-10-131-827-2395
; Sequence 2395, Application US/10131827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2395
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2395

Query Match 74.4%; Score 13.4; DB 6; Length 50;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 gagcactaaagctgg 18
||| ||||| |||
Db 17 gagaactaaagctgg 31

RESULT 5
US-10-019-906-16
; Sequence 16, Application US/10019906
; GENERAL INFORMATION:
; APPLICANT: Richardson, Peter
; APPLICANT: Cox, Peter
; TITLE OF INVENTION: A Method for Amplifying Low Abundance Nucleic Acid Sequences a
; FILE REFERENCE: GJE-83
; CURRENT APPLICATION NUMBER: US/10/019,906
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/144,666
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-019-906-16

Query Match 73.3%; Score 13.2; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18
||| ||| || ||||| |||
Db 1 tctgaccacaagctgg 18

RESULT 6
US-10-019-906A-16
; Sequence 16, Application US/10019906A
; GENERAL INFORMATION:
; APPLICANT: Richardson, Peter
; APPLICANT: Cox, Peter
; TITLE OF INVENTION: A Method for Amplifying Low Abundance Nucleic Acid Sequences a
; FILE REFERENCE: GJE-83
; CURRENT APPLICATION NUMBER: US/10/019,906A
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/144,666
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: oligonucleotide
US-10-019-906A-16

Query Match 73.3%; Score 13.2; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18
||||| ||| |||||

Db 1 tctgaccacaagaagctgg 18

RESULT 7

US-09-956-604-12259

; Sequence 12259, Application US/09956604

; GENERAL INFORMATION:

; APPLICANT: Mitmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli

; FILE REFERENCE: 3117.1

; CURRENT APPLICATION NUMBER: US/09/956,604

; CURRENT FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/234,049

; PRIOR FILING DATE: 2000-09-19

; NUMBER OF SEQ ID NOS: 141629

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 12259

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Escherichia coli

US-09-956-604-12259

Query Match 73.3%; Score 13.2; DB 5; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18
||||| |||||

Db 4 tcttaagactaaagctgg 21

RESULT 8

US-09-956-604-107078

; Sequence 107078, Application US/09956604

; GENERAL INFORMATION:

; APPLICANT: Mitmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli

; FILE REFERENCE: 3117.1

; CURRENT APPLICATION NUMBER: US/09/956,604

; CURRENT FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/234,049

; PRIOR FILING DATE: 2000-09-19

; NUMBER OF SEQ ID NOS: 141629

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 107078

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Escherichia coli

US-09-956-604-107078

Query Match 72.2%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 gcactaaagctgg 18
||||| |||||

Db 5 gcactaaagctgg 17

RESULT 9

US-10-027-632-176505/c

; Sequence 176505, Application US/10027632
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 176505

; LENGTH: 23

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-176505

Query Match 71.1%; Score 12.8; DB 7; Length 23;

Best Local Similarity 87.5%; Pred. No. 2.5e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagct 16
||||| |||||

Db 17 TCTGAGCACACAGCT 2

RESULT 10

US-09-396-196G-53894/c

; Sequence 53894, Application US/09396196G

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 53894

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-53894

Query Match 71.1%; Score 12.8; DB 5; Length 25;

Best Local Similarity 87.5%; Pred. No. 2.6e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagct 16
||||| |||||

Db 20 TCTGAGCTCTACAGCT 5

RESULT 11

US-09-396-196G-69541
; Sequence 69541, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-69541

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagctg 17
||| || |||||

Db 5 ctgtgcgctaaagctg 20

RESULT 12
US-09-396-196G-84670/c
; Sequence 84670, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84670
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-84670

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgagcactaaagctg 18
||||| |||||

Db 25 TGAGCACAATAATGG 10

RESULT 13
US-09-396-196G-105745
; Sequence 105745, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-105745

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctgagcactaaagct 16
||||| |||||

Db 5 tctgagcactataact 20

RESULT 14
PCT-US01-44838-533/c
; Sequence 533, Application PC/TUS0144838
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; TITLE OF INVENTION: Genetic Typing of Human Genes And Related Materials And Method
; FILE REFERENCE: 4389-23-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/44838
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 1449
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 533
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-44838-533

Query Match 68.9%; Score 12.4; DB 1; Length 20;
Best Local Similarity 92.9%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctgagcactaaag 14
||||| |||||

Db 15 TCTGAGCACAATAATG 2

RESULT 15
US-09-396-196G-117149/c
; Sequence 117149, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117149
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-117149

Query Match 68.9%; Score 12.4; DB 5; Length 25;
Best Local Similarity 92.9%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tctgagcactaaag 14
 |||||
Db 24 TCTGAGCAGGAAG 11

Search completed: October 12, 2002, 17:27:28
Job time: 10803 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:51:13 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: US-09-945-131-3
Perfect score: 18
Sequence: 1 gtgatagatgccgagca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *

- 1: gb_ba:*
- 2: gb_hlg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
------------	-------	-------	--------	----	-------------

c	1	13.8	76.7	45	9	S54891	S54891 T-cell rece
c	2	12.2	67.8	20	6	AX080276	AX080276 Sequence
c	3	12.2	67.8	21	6	AX111202	AX111202 Sequence
c	4	12.2	67.8	37	6	AR008967	AR008967 Sequence
c	5	12	66.7	27	6	AR143811	AR143811 Sequence
c	6	11.6	64.4	30	6	AX100540	AX100540 Sequence
c	7	11.4	63.3	30	6	AX17582	AX17582 Oligonucleo
c	8	11.4	63.3	36	9	HSTCARB2	HSTCARB2 H.sapiens (
c	9	11.4	63.3	45	6	E60002	E60002 Ceramide-bi
c	10	11.4	63.3	45	10	MUSTCRBCAB	MUSTCRBCAB Mouse T-cel
c	11	11.2	62.2	19	6	AX354589	AX354589 Sequence
c	12	11.2	62.2	20	6	AX057501	AX057501 Sequence
c	13	11.2	62.2	20	6	AX119428	AX119428 Sequence
c	14	11.2	62.2	20	6	AX119528	AX119528 Sequence
c	15	11.2	62.2	21	6	AR091447	AR091447 Sequence
c	16	11.2	62.2	24	6	I26952	I26952 Sequence 1
c	17	11.2	62.2	24	6	I28388	I28388 Sequence 1
c	18	11.2	62.2	24	6	I96080	I96080 Sequence 1
c	19	11.2	62.2	25	6	I33604	I33604 Sequence 26
c	20	11.2	62.2	27	6	AR047936	AR047936 Sequence
c	21	11.2	62.2	28	6	AX057466	AX057466 Sequence
c	22	11.2	62.2	30	6	AX2595	AX2595 Sequence 11
c	23	11.2	62.2	30	6	AB8783	AB8783 Sequence 93
c	24	11.2	62.2	30	6	AR001285	AR001285 Sequence
c	25	11.2	62.2	30	6	AR003602	AR003602 Sequence
c	26	11.2	62.2	30	6	AR025286	AR025286 Sequence
c	27	11.2	62.2	30	6	AR037092	AR037092 Sequence
c	28	11.2	62.2	30	6	AR063120	AR063120 Sequence
c	29	11.2	62.2	30	6	AR063123	AR063123 Sequence
c	30	11.2	62.2	30	6	AR164690	AR164690 Sequence
c	31	11.2	62.2	30	6	I24824	I24824 Sequence 6
c	32	11.2	62.2	30	6	I35448	I35448 Sequence 15
c	33	11.2	62.2	31	6	AX248210	AX248210 Sequence
c	34	11.2	62.2	34	6	AR044274	AR044274 Sequence
c	35	11.2	62.2	34	6	I35914	I35914 Sequence 15
c	36	11.2	62.2	34	6	I68887	I68887 Sequence 15
c	37	11.2	62.2	45	6	AR026954	AR026954 Sequence
c	38	11.2	62.2	45	10	MMU400649	MMU400649 Mus muscu
c	39	11.2	62.2	48	6	AR044207	AR044207 Sequence
c	40	11.2	62.2	48	6	AR044208	AR044208 Sequence
c	41	11.2	62.2	48	6	I35847	I35847 Sequence 47
c	42	11.2	62.2	48	6	I35848	I35848 Sequence 48
c	43	11.2	62.2	49	9	HUMTFCOF25	HUMTFCOF25 Human putat
c	44	10.8	60.0	15	6	AX343385	AX343385 Sequence
c	45	10.8	60.0	17	6	AX227282	AX227282 Sequence

ALIGNMENTS

RESULT	1	S54891	45 bp	mrna	linear	PRI 22-JUN-1993
LOCUS		S54891				
DEFINITION		S54891				
ACCESSION		S54891				
VERSION		S54891.1				
KEYWORDS		human T lymphocytes.				
SOURCE		human T lymphocytes.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
TITLE		1 (bases 1 to 45)				
JOURNAL		Shimonkevitz, R., Colburn, C., Burnham, J.A., Murray, R.S. and				
MEDLINE		Kotzin, B.L.				
REMARK		Clonal expansions of activated gamma/delta T cells in recent-onset				
FEATURES		Multiple sclerosis				
		Proc. Natl. Acad. Sci. U.S.A. 90 (3), 923-927 (1993)				
		93157384				
		GenBank staff at the National Library of Medicine created this				
		entry [NCBI gibbsq 124257] from the original journal article.				
		This sequence comes from Fig. 2.				
		Location/Qualifiers				

3

```

RESULT 6
AX100540/c
LOCUS AX100540 30 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 5 from Patent WO0121785.
ACCESSION AX100540
VERSION AX100540.1 GI:13619544
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE
1 (bases 1 to 30)
AUTHORS Jefferson,R.A., Yang,W. and Grossnicklaus,U.
TITLE Megagametophyte transcriptional control elements and uses thereof
JOURNAL Patent: WO 0121785-A 5 29-MAR-2001;
Cambia (AU); COLD SPRING HARBOR LABORATORY (US); JEFFERSON,
Richard Anthony (AU); Yang, Wei (AU); Grossnicklaus, Ueli (CH)
FEATURES
source
1..30
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
misc_feature 1..30
BASE COUNT 10 a 9 c 4 g 7 t
ORIGIN
Query Match 64.4%; Score 11.6; DB 6; Length 30;
Best Local Similarity 77.8%; Pred. No. 5.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 gtgatagatgccgagca 18
||||| ||| |||
Db 27 GTGATATTAGCTAAGCA 10

RESULT 7
AX17582
LOCUS AX17582 30 bp DNA linear PAT 23-MAR-1994
DEFINITION Oligonucleotide primer OBVD 8 location on BVDV genome 1808 - 1837.
ACCESSION AX17582
VERSION AX17582.1 GI:513082
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE
1 (bases 1 to 30)
AUTHORS Belak,S. and Ballagi-Pordany,A.
TITLE A method of detecting an infection caused by a specific type of
virus, primers, probes and a test kit
JOURNAL Patent: EP 0464010-A 6 02-JAN-1992;
STATENS VETERINAERMEDICINSKA ANSTALT
FEATURES
source
1..30
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 3 a 10 c 5 g 12 t
ORIGIN
Query Match 63.3%; Score 11.4; DB 6; Length 30;
Best Local Similarity 92.3%; Pred. No. 7.5e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 tagtatgccgagc 17
||||| |||
Db 10 TAGTATCCCGAGC 22

RESULT 8
HSTCARB2
LOCUS HSTCARB2 36 bp mRNA linear PRI 28-JUN-1995

```

```

DEFINITION H.sapiens (BDE20) mRNA for T-cell antigen receptor-beta.
ACCESSION Z35671
VERSION Z35671.1 GI:527467
KEYWORDS T-cell antigen receptor-beta.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 36)
AUTHORS Lehner,P.J.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1994) Paul J. Lehner Dr., Medicine, Tenovus
Building, University of, Wales College of Medicine, Heath Park,
Cardiff, South Glamorgan, CF4 4XN, Wales, UK
REFERENCE
2 (bases 1 to 36)
AUTHORS Lehner,P.J., Wang,E.C., Moss,P.A., Williams,S., Platt,K.,
Friedman,S.M., Bell,J.I. and Borysiewicz,L.K.
TITLE Human HLA-A*0201-restricted cytotoxic T lymphocyte recognition of
Influenza A is dominated by T cells bearing the V beta 17 gene
segment
JOURNAL J. Exp. Med. 181 (1), 79-91 (1995)
MEDLINE 95105732
FEATURES
source
1..36
Location/Qualifiers
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/isolate="BD"
/db_xref="taxon:9606"
/clone="BDE20"
/cell_type="cytotoxic T lymphocyte"
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/codon_start=1
/product="T-cell antigen receptor VJ junction beta chain"
/protein_id="CAA84740.1"
/db_xref="GI:527468"
/translaton="CASSMRSSSQHF"
misc_feature 9..30
BASE COUNT 7 a 9 c 11 g 9 t
ORIGIN
Query Match 63.3%; Score 11.4; DB 9; Length 36;
Best Local Similarity 92.3%; Pred. No. 7.5e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 tagtatgccgagc 17
||||| |||
Db 9 TAGTATCGGAGC 21

RESULT 9
E60002/c
LOCUS E60002 45 bp DNA linear PAT 31-JAN-2002
DEFINITION Ceramide-binding peptide.
ACCESSION E60002
VERSION E60002.1 GI:18622761
KEYWORDS JP 2000319296-A/2
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE
1 (bases 1 to 45)
AUTHORS Ishikawa,M., Tanaka,Y., Ogino,K. and Taki,T.
TITLE Ceramide-binding peptide
JOURNAL Patent: JP 2000319296-A 2 21-NOV-2000;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Artificial Sequence
PN JP 2000319296-A/2
PD 21-NOV-2000
PF 10-MAY-1999 JP 1999128674
PI MASARU ISHIKAWA,YOSHINORI TANAKA,KOICHI OGINO,TAKAO TAKI PC
CC C07K7/00

```


KEYWORDS SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nfl gene
JOURNAL Patent: WO 0129251-A 85 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 5 a 2 c 7 g 6 t
ORIGIN
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2 ||| ||||| |||
3 GTTATTGTATCGGAG 18
Query Match 62.2%; Score 11.2; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 gtgatatgtatgccgag 16
||| ||||| |||
Db 3 GTTATTGTATCGGAG 18
RESULT 14
AX119528
LOCUS AX119528 20 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 185 from Patent WO0129251.
ACCESSION AX119528
VERSION AX119528.1 GI:14036447
KEYWORDS human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nfl gene
JOURNAL Patent: WO 0129251-A 185 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 5 a 2 c 7 g 6 t
ORIGIN
1 ||| ||||| |||
2 ||| ||||| |||
3 GTTATTGTATCGGAG 18
Query Match 62.2%; Score 11.2; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 gtgatatgtatgccgag 16
||| ||||| |||
Db 3 GTTATTGTATCGGAG 18
RESULT 15
AR091447
LOCUS AR091447 21 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 11 from patent US 5994119.
ACCESSION AR091447
VERSION AR091447.1 GI:10018202
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dietz,H.C.
TITLE Mammalian regulator of nonsense-mediated RNA decay

JOURNAL Patent: US 5994119-A 11 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..21
BASE COUNT 5 a 5 c 7 g 4 t
ORIGIN
1 ||| ||||| |||
2 ||| ||||| |||
3 GTTATTGTATCGGAG 18
Query Match 62.2%; Score 11.2; DB 6; Length 21;
Best Local Similarity 81.2%; Pred. No.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 tgatatgtatgccgagc 17
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Db 4 TCACAGGATGCAGAGC 19
Search completed: October 12, 2002, 16:51:15
Job time: 8890 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:01 ; Search time 792.17 Seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-3

Perfect score: 18
Sequence: 1 gtgatagtagtcgcgagca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*

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- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AA13834	Murine PDGFR-beta
2	12.8	71.1	47	AA094496	Human antibody ONS
3	12.8	71.1	47	AAT38611	Chimaeric human/mu
4	12.2	67.8	20	AAF63623	Isogenic transgeni
5	12.2	67.8	21	AAH01942	parC resistance ge
6	12.2	67.8	37	AAH01544	Antisense primer f
7	12	66.7	21	AAV51618	Zea mays genome fo
8	12	66.7	27	AA227099	Saccharomyces cere
9	11.8	65.6	21	AAH40980	CAP marker primer

10	11.8	65.6	46	21	AA151720	PCR primer 194-89
11	11.6	64.4	25	24	ABK16565	Short tandem repea
12	11.6	64.4	30	22	AAF77637	A thaliana enhance
13	11.6	64.4	34	22	AAJ16133	Human VEGF-B10-108
14	11.6	64.4	42	22	AAH41016	PCR primer specifi
15	11.6	64.4	47	21	AAZ67522	Human map-related
16	11.4	63.3	26	17	AAO3660	Osteoblast prolife
17	11.4	63.3	30	13	AAO20364	Primer OBVD8 from
18	11.4	63.3	45	22	AAF25920	Ceramide affinity
19	11.2	62.2	19	24	AAZ4330	Human Stat1 amplif
20	11.2	62.2	20	22	AAO4985	Neurofibromatosis
21	11.2	62.2	20	22	AAO5085	Neurofibromatosis
22	11.2	62.2	20	22	AAO4801	Human TLR4 gene ex
23	11.2	62.2	21	18	AAT96720	Human RENT1 primer
24	11.2	62.2	24	13	AAO29498	EDA-FN primer (1).
25	11.2	62.2	25	18	AAT59971	Primer PC24 for P.
26	11.2	62.2	27	16	AAT04253	Primer #1 for TA a
27	11.2	62.2	28	22	AAZ4770	Human TLR4 exon 2/
28	11.2	62.2	29	15	AAO5954	COL2A1 3'-primer (
29	11.2	62.2	30	16	AAO3378	c-fos antisense ol
30	11.2	62.2	33	24	ABA05584	Human Pax protein
31	11.2	62.2	39	21	AAA26591	Human HPC1 mutatio
32	11.2	62.2	41	22	AAI65255	Human dihydroorota
33	11.2	62.2	45	16	AAQ75899	CDR-grafting prime
34	11.2	62.2	50	22	AAI28257	Human SNP oligonuc
35	11	61.1	12	23	AB144725	Oligonucleotide pr
36	11	61.1	19	15	AAQ57322	Enzymatic RNA mole
37	11	61.1	25	21	AAH82987	HHV6 detecting PCR
38	11	61.1	25	22	AAH03056	Microorganism dete
39	11	61.1	28	20	AAH35844	Antisense oligonuc
40	10.8	60.0	17	22	AAH95229	Human Chk1 ribozym
41	10.8	60.0	17	22	AAH95518	Human Chk1 ribozym
42	10.8	60.0	17	22	AAH95729	Human Chk1 ribozym
43	10.8	60.0	17	22	AAH95978	Human Chk1 ribozym
44	10.8	60.0	19	22	AAF54544	Primer #148 used i
45	10.8	60.0	20	20	AAH93233	PCR primer used to

ALIGNMENTS

RESULT 1
AA13834
ID AAA13834 standard; DNA; 18 BP.

XX AAA13834;

AC AAA13834;

DT 27-JUL-2000 (first entry)

XX Murine PDGFR-beta scrambled control oligonucleotide SEQ ID NO:3.

XX Murine; mouse; platelet derived growth factor receptor beta; vasotropic;

XX PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;

XX recurrent stenosis; cardiovascular injury; ss.

XX Mus sp.

XX Key modified_base Location/Qualifiers

FT 1..18 /*tag= a

FT /note= "phosphorothioate linkages"

XX CA2228977-A1.

XX 07-MAY-1999.

XX 03-FEB-1998; 98CA-2228977.

XX 07-NOV-1997; 97CA-2215360.

XX (EDEL/) EDELMAN E R.

XX (ROSE/) ROSENBERG R D.

XX (SIRO/) SIROIS M G.

PA (SIMO/) SIMONS M.
 XX Edelman ER, Rosenberg RD, Sirois MG, Simons M;
 XX WPI; 2000-283933/25.
 XX Antisense inhibition of platelet derived growth factor beta-receptor
 PT subunit expression for the prevention of restenosis -
 XX Example 1; Page 15; 43pp; English.
 XX A method has been developed for preventing restenosis following vascular
 CC injury by antisense inhibition of platelet derived growth factor
 CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
 CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
 CC canal), especially of a valve in the heart, after surgical correction of
 CC the primary condition) following cardiovascular injury. The present
 CC sequence represents a scrambled control phosphorothioate oligonucleotide
 CC for murine PDGFR-beta, which is used in an example from the present
 CC invention.
 XX Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.57; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgatatgtagccgagca 18
 ||||| ||||| ||||| |||||
 Db 1 gtgatatgtagccgagca 18

RESULT 2
 AAQ94496
 ID AAQ94496 standard; DNA; 47 BP.
 XX
 AC AAQ94496;
 XX
 DT 16-JAN-1996 (first entry)
 XX
 DE Human antibody ONS-M21 CDR PCR primer F.
 XX
 KW Human; ONS-M21 antibody; chimeric protein; CDR; medulloblastoma;
 KW brain tumour; treatment; diagnosis; PCR primer F;
 KW complementarity determining region; ss.
 XX
 OS Synthetic.
 XX
 PN W09514041-A1.
 XX
 PD 26-MAY-1995.
 XX
 PF 19-OCT-1994; 94WO-JP01763.
 XX
 PR 19-NOV-1993; 93JP-0291078.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ohtomo T, Sato K, Tsuchiya M;
 XX
 DR WPI; 1995-200347/26.
 XX
 XX Reconstituted antibody against human medullo:blastoma cells -
 PT contains high proportion of human antibody origin and has low
 PT antigenicity
 XX
 PS Example 5; Page 63; 120pp; Japanese.
 XX
 CC AAQ94492-Q94497 are human antibody ONS-M21 CDR PCR primers. The
 CC cDNA encoding the CDRs was used in the construction of an
 CC expression vector, contg. cDNA encoding a human/murine chimeric
 CC antibody, reactive with human medulloblastoma (a brain tumour)

CC cells. The chimeric antibody can be used in the diagnosis and
 CC treatment of this disease.
 XX
 SQ Sequence 47 BP; 12 A; 12 C; 14 G; 9 T; 0 other;
 Sequence 47 BP; 12 A; 12 C; 14 G; 9 T; 0 other;
 Indels 0; Gaps 0;

Query Match 71.1%; Score 12.8; DB 16; Length 47;
 Best Local Similarity 87.5%; Pred. No. 7.2e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gatagtatgccgagca 18
 ||||| ||||| ||||| |||||
 Db 17 gatagtatgccgagta 32

RESULT 3
 AAT38611
 ID AAT38611 standard; DNA; 47 BP.
 XX
 AC AAT38611;
 XX
 DT 09-DEC-1996 (first entry)
 XX
 DE Chimaeric human/murine MAB ONS-M21 PCR primer G.
 XX
 KW Murine; human; myeloblastoma; chimaera; monoclonal antibody;
 KW chimera; single stranded Fv region; PCR; low human antigenicity;
 KW diagnosis; treatment; cerebral tumour; reshaped; primer;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN JP08169900-A.
 XX
 PD 02-JUL-1996.
 XX
 PF 18-NOV-1994; 94JP-0285057.
 XX
 PR 18-OCT-1994; 94JP-0252166.
 PR 19-NOV-1993; 93JP-0291078.
 XX
 PA (CHUS) CHUGAI PHARM CO LTD.
 XX
 DR WPI; 1996-358509/36.
 XX
 PT Reshaped anti-human myeloblastoma cell human antibody - has low
 PT human antigenicity, and is therefore useful for diagnosis and
 PT treatment of cerebral tumours, e.g. myeloblastoma
 XX
 PS Example 5; Page 23; 45pp; Japanese.
 XX
 CC The present sequence is a primer for the chimaeric human/murine
 CC monoclonal antibody (MAB) ONS-M21. The MAB was prepd. by combining
 CC light and heavy variable region DNA, from a murine anti-human
 CC myeloblastoma cell MAB, with human light and heavy constant region
 CC sequences, respectively to produce chimaeric human/murine light and
 CC heavy chain DNA mols.. A recombinant vector for the expression of
 CC the heavy and light chain DNA mols. was prepd., and used to
 CC transform a host cell. The host cell was then cultured, and the
 CC expression prods. of the heavy and light chain DNA mols. sepd. and
 CC connected with a peptide linker to produce a single stranded Fv
 CC region. The reshaped Fv region has low human antigenicity, and is
 CC therefore expected to be useful as an agent for the diagnosis and
 CC treatment of cerebral tumours, e.g. myeloblastoma.
 XX
 SQ Sequence 47 BP; 12 A; 12 C; 14 G; 9 T; 0 other;

Query Match 71.1%; Score 12.8; DB 17; Length 47;
 Best Local Similarity 87.5%; Pred. No. 7.2e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gatagtatgccgagca 18

QY 1 gtgatagtatgccgagc 17
 || |||||
 Db 18 GTCGAAGTATGCCGAGC 2

RESULT 6
 AAQ81544
 ID AAQ81544 standard; cDNA; 37 BP.

XX AC AAQ81544;

XX DT 07-OCT-1995 (first entry)

XX DE Antisense primer for adeno virus 5 fiber sequence.

XX KW DNA primer; adeno virus; ss; CD30 ligand; Hodgkins lymphoma;
 XX KW gene therapy.

XX OS Synthetic.

XX PN W09505201-A.

XX PD 23-FEB-1995.

XX PF 11-AUG-1994; 94WO-US09172.

XX PR 13-AUG-1993; 9305-0106078.

XX PA (GENE-) GENETIC THERAPY INC.

XX PI McClelland A, Stevenson SC;

XX DR WPI; 1995-098586/13.

XX PT Adenovirus comprising fibre protein contg. a ligand - specific
 XX PT for cell surface receptor, used to treat Hodgkin's lymphoma.

XX PS Example 4; Page 29; 71pp; English.

XX CC The DNA primer, specific for the adeno virus 5 fiber gene, is used
 CC with sense primer AAQ81543 in the construction of plasmid p680.2
 CC containing adeno virus 5 fiber genes. This plasmid can be used to
 CC direct substitutions of modified adeno virus 5 fiber genes into YAC,
 CC and ultimately in the construction of plasmid pGEM5r:CD30L and a
 CC recombinant adeno virus expressing a 5F:CD30 ligand chimera. The
 CC recombinant adeno virus vector is used for in vivo transduction of
 CC cells expressing the LDL receptor e.g. liver cells, for CD30 ligand
 CC gene expression in vivo. Preferably, adeno virus 5 has residues
 CC 400-581 replaced with CD30 ligand cDNA. This process is used for the
 CC treatment of Hodgkins lymphoma, adenosine-deaminase deficiency,
 CC sickle cell anaemia, thalassaemia, alpha-antitrypsin deficiency,
 CC Alzheimer disease, phenylketonuria, growth disorders and heart
 CC disease by gene therapy.

XX SQ Sequence 37 BP; 11 A; 10 C; 9 G; 7 T; 0 other;

Query Match 67.8%; Score 12.2; DB 16; Length 37;
 Best Local Similarity 82.4%; Pred. No. 1.6e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tgatagtatgccgagca 18
 ||||| |||||
 Db 21 tgatcatcatgacgagca 37

RESULT 7
 AAV51618
 ID AAV51618 standard; DNA; 21 BP.

XX AC AAV51618;

XX XX 02-FEB-1999 (first entry)

XX Zea mays genome forward PCR primer #218.

XX DE Polymorphic marker; allele-specific; probe; amplification; PCR primer;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; corn; ss.

XX OS Synthetic.

XX OS Zea mays.

XX PN W09824796-A1.

XX PD 11-JUN-1998.

XX PF 01-DEC-1997; 97WO-US21782.

XX PR 07-MAR-1997; 97US-0813507.

XX PR 02-DEC-1996; 96US-0032069.

XX PA (AFFY-) AFFYMETRIX INC.

XX XX Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;

XX DR WPI; 1998-333252/29.

XX CC Brassica species allele-specific oligonucleotide probes and primers

XX PS - useful for plant breeding

XX XX Example 1; Page Page 53; 65pp; English.

XX CC AAV51401-V51704 are forward PCR primers used to amplify fragments of the
 CC Zea mays genome in order to detect polymorphic markers. Such markers can
 CC be used in the construction of allele-specific primers and probes for
 CC amplification or hybridisation, e.g. to determine common or disparate
 CC ancestry between 2 or more plants, to monitor the genetic contribution
 CC of an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a
 CC back-crossed plant with an ancestral plant.

XX SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 other;

Query Match 66.7%; Score 12; DB 19; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 agtatgccgagc 17

Db ||||| |||||

6 agtatgccgagc 17

RESULT 8

AAZ27099/C

ID AAZ27099 standard; DNA; 27 BP.

XX AC AAZ27099;

XX XX 19-NOV-1999 (first entry)

XX DE Saccharomyces cerevisiae DNA-binding protein target sequence #70.

XX KW DNA binding protein; DBP; zinc finger; 2F domain; target; ss.

XX OS Saccharomyces cerevisiae.

XX PN W09942474-A2.

XX PD 26-AUG-1999.

XX PF 19-FEB-1999; 99WO-US03692.

XX XX 20-FEB-1998; 98US-0075466.

XX XX

SQ Sequence 46 BP; 18 A; 5 C; 14 G; 9 T; 0 other;

Query Match 65.6%; Score 11.8; DB 21; Length 46;
Best Local Similarity 86.7%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtgatagatgccga 15
||||| ||||| |||
Db 19 gtgatcgtatgacga 33

RESULT 11

ABK16565/c
ID ABK16565 standard; DNA; 25 BP.

XX ABK16565;

AC ABK16565;

XX 14-MAR-2002 (first entry)

XX Short tandem repeat loci detection, multiplex PCR primer #42.

DE Multiplex PCR; short tandem repeat; STR; amelogenin;

KW Combined DNA index system; CODIS; PCR primer;

KW locus specific bracket; LSB; locus specific allelic ladder; ss.

XX Synthetic.

XX WO200192575-A1.

PN 06-DEC-2001.

XX 23-MAY-2001; 2001WO-US16547.

XX 30-MAY-2000; 2000US-0580497.

PR (OLIG-) OLIGOTRAIL LLC.

XX Dau PC, Liu D;

XX WPI; 2002-090048/12.

XX Determining the alleles at several loci in a DNA-containing sample,

PT useful for analysing short tandem repeat genetic markers in a genomic

PT system, by multiplex PCR of thirteen Combined DNA Index System (CODIS)

PT loci and amelogenin

XX Claim 18; Page 33; 164pp; English.

XX The invention describes a novel method of determining the alleles

CC present at several loci in a DNA-containing sample. The method comprises

CC amplifying by multiplex PCR the thirteen specific and distinct

CC polymorphic short tandem repeat (STR) genetic loci of the Combined DNA

CC Index System (CODIS) and amelogenin for sex determination. The method is

CC useful for detecting and analysing short tandem repeat (STR) genetic

CC markers in a genomic system. The length of amplified alleles can be

CC determined using both internal and external lane calibration standards,

CC including locus specific brackets (LSB) and locus specific allelic

CC ladders respectively. This sequence is one of 43 PCR primers

CC (ABK16524-ABK16566) designed to amplify the STR's in a genomic sample,

CC described in the method of the invention.

XX Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 other;

Query Match 64.4%; Score 11.6; DB 24; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtgatagatgccga 18
||||| ||||| |||
Db 18 GTGATACCATGTCCAGCA 1

RESULT 12

AAF77637/c
ID AAF77637 standard; DNA; 30 BP.

XX AAF77637;

AC AAF77637;

XX 29-MAY-2001 (first entry)

XX A thaliana enhancer element PCR primer SEQ ID NO: 5.

XX Megagametophyte transcriptional control element; enhancer element;

KW female gametophyte specific gene expression; cereal; PCR primer; ss.

XX Arabidopsis thaliana.

XX WO200121785-A2.

PN 29-MAR-2001.

XX 20-SEP-2000; 2000WO-US26359.

XX 20-SEP-1999; 99US-0155361.

PR (CMB-) CAMBIA.

XX (COLD-) COLD SPRING HARBOR LAB.

PA (JEFF/) JEFFERSON R A.

PA (YANG/) YANG W.

PA (GROS/) GROSSNICKLAUS U.

XX Jefferson RA, Yang W, Grossnicklaus U;

PI WPI; 2001-257983/26.

XX New plant transformation vector for expression of structural genes,

PT comprises an enhancer element operably linked to a nucleotide sequence

PT of interest, operative in a plant megagametophyte

XX Example 3; Page 41; 48pp; English.

XX The present invention describes a plant transformation vector comprising

CC an enhancer element operative in a plant megagametophyte, where the

CC enhancer is operably linked to a coding sequence of interest. This is

CC useful for promoting the expression of sequences of interest in the

CC female gametophyte only, particularly in cereals such as rice.

XX Sequence 30 BP; 10 A; 9 C; 4 G; 7 T; 0 other;

Query Match 64.4%; Score 11.6; DB 22; Length 30;
Best Local Similarity 77.8%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtgatagatgccga 18
||||| ||||| |||
Db 27 GTGATATTAGGCTAAGCA 10

RESULT 13

AAD16133/c
ID AAD16133 standard; DNA; 34 BP.

XX AAD16133;

XX 19-NOV-2001 (first entry)

XX Human VEGF-B10-108 mature DNA amplifying 5' primer.

DE Protein purification; affinity chromatography; angiogenesis;

XX vascular endothelial growth factor; autotransplantation; tumour;

KW rheumatoid arthritis; diabetic retinopathy; human;

KW VEGF-B10-108; PCR primer; ss.

XX

```

OS Homo sapiens.
PN WO200160861-A1.
XX
XX 23-AUG-2001.
PD
XX
XX 16-FEB-2001; 2001WO-AU00160.
XX PF
XX 16-FEB-2000; 2000AU-0005681.
XX PR
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
PA
XX
XX Scrofani SDB, Nash AD, Fabri LJ, Mackenzie AW, Scotney PD;
PI
XX WPI; 2001-541645/60.
DR
XX Purifying a protein or polypeptide, e.g. vascular endothelial growth
PT factor (VEGF)-B isoform, comprises subjecting a biological sample to
PT affinity chromatography to allow the full length to bind and not the
PT truncated or clipped forms -
XX
XX Example 21; Page 36; 77pp; English.
PS
XX The invention relates to a method for purifying a polypeptide comprising
CC subjecting a biological sample to chromatography with an affinity matrix
CC for an N- or C-terminal region of the polypeptide, that permits binding
CC of full length molecule and not the truncated form. The method is useful
CC for purifying human vascular endothelial growth factor (VEGF) especially
CC VEGF-B isoforms e.g. VEGF-B167, VEGF-B186 and VEGF-B108. VEGF is
CC involved in normal angiogenesis including formation of the corpus luteum,
CC placental development, regulation of vascular permeability, inflammatory
CC angiogenesis, autotransplantation and human diseases such as tumour
CC promoting angiogenesis, rheumatoid arthritis and diabetes related
CC retinopathy. The VEGF molecules are useful in therapeutic protocols and
CC diagnostic assays. The present sequence is a PCR primer used for
CC amplifying mature human VEGF-B10-108 DNA.
XX
XX Sequence 34 BP; 12 A; 11 C; 8 G; 3 T; 0 other;
SQ
Query Match 64.4%; Score 11.6; DB 22; Length 34;
Best Local Similarity 77.8%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 gtgatagtatgccgagca 18
Db 24 GTGATAGTGTGCTGCGGA 7
RESULT 14
AAH41016/C
ID AAH41016 standard; DNA; 42 BP.
XX
XX AAH41016;
AC
XX 23-AUG-2001 (first entry)
DT
XX PCR primer specific for human metalloprotease DNA.
DE
XX Metalloprotease; human; aggrecanase; joint disease; osteoarthritis;
KW osteopathic; antiarthritic; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200134785-A1.
PN
XX 17-MAY-2001.
PD
XX 10-NOV-2000; 2000WO-JP07917.
XX PF
XX 11-NOV-1999; 99JP-0321740.
XX PR
XX 16-MAY-2000; 2000JP-0144020.
XX
PA (YAMA ) YAMANOUCHI PHARM CO LTD.
PA (KAZU-) KAZUSA DNA RES INST.
XX
XX Yamaji N, Nishimura K, Abe K, Ohara O, Nagase T, Nomura N;
PI
XX WPI; 2001-343602/36.
XX
XX Metalloprotease with aggrecanase activity for treating joint diseases
PT especially osteoarthritis -
PT
XX Example 4; Page 62; 85pp; Japanese.
PS
XX This invention relates to a metalloprotease with aggrecanase activity.
CC The invention includes protein and DNA sequences of the metalloprotease,
CC vectors containing the DNA, host cells transformed by the vectors, and
CC antibodies directed against the metalloprotease. The antibodies, protein
CC and DNA sequences can be used in the treatment and prevention of joint
CC diseases, particularly osteoarthritis. The treatment may result in
CC osteopathic and antiarthritic activity. The present sequence represents
CC a PCR primer used in the isolation and characterisation of the
CC metalloprotease gene of the invention.
XX
XX Sequence 42 BP; 6 A; 12 C; 11 G; 13 T; 0 other;
SQ
Query Match 64.4%; Score 11.6; DB 22; Length 42;
Best Local Similarity 77.8%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 gtgatagtatgccgagca 18
Db 37 GGGTTAGGATGCCAGCA 20
RESULT 15
AAZ67522
ID AAZ67522 standard; DNA; 47 BP.
XX
XX AAZ67522;
AC
XX 10-SEP-2001 (first entry)
DT
XX Human map-related biallelic marker SEQ ID NO:1869.
DE
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
OS
XX
XX Key variation Location/Qualifiers
FH replace(24,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO9954500-A2.
PN
XX 28-OCT-1999.
PD
XX 21-APR-1999; 99WO-IB00822.
XX PF
XX 21-APR-1998; 98US-0082614.
XX PR 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
PA
XX Cohen D, Blumenfeld M, Chumakov I;
PI
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -

```

Claim 1; Page 629; 2745pp; English.

AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention.

Sequence 47 BP; 17 A; 7 C; 12 G; 11 T; 0 other;

-Query Match	64.4%;	Score 11.6;	DB 21;	Length 47;
Best Local Similarity	77.8%;	Pred. No. 3.6e+03;		
Matches 14;	Conservative	0;	Mismatches 4;	Indels 0;
Qy	1	gtgatagatgccgagca	18	
Db	22	qqaaagtatgctgaqaa	39	

Search completed: October 12, 2002, 17:08:02
Job time: 9747 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:35 ; Search time 191.26 seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-3

Perfect score: 18

Sequence: 1 gtgatagtagcgagca 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.8	71.1	47	4	US-08-646-265A-40
2	12.2	67.8	37	1	US-08-591-492-16
3	12	66.7	27	4	US-09-253-396A-73
4	11.8	65.6	46	3	US-09-235-246-16
5	11.4	63.3	26	3	US-08-604-965E-14
6	11.4	63.3	26	3	US-08-604-965E-20
7	11.2	62.2	21	2	US-08-724-354D-11
8	11.2	62.2	21	3	US-09-270-984A-11
9	11.2	62.2	24	1	US-08-244-494A-1
10	11.2	62.2	24	1	US-08-119-231-1
11	11.2	62.2	24	1	US-08-628-343-1
12	11.2	62.2	25	1	US-08-448-204-26
13	11.2	62.2	27	1	US-08-207-481-13
14	11.2	62.2	27	5	PCT-US95-02689-13
15	11.2	62.2	30	1	US-07-789-179-6
16	11.2	62.2	30	1	US-08-240-712-15
17	11.2	62.2	30	1	US-08-443-890-15
18	11.2	62.2	30	1	US-08-444-942-6
19	11.2	62.2	30	1	US-08-446-105-6
20	11.2	62.2	30	1	US-08-444-939-6
21	11.2	62.2	30	2	US-08-444-991-6
22	11.2	62.2	30	2	US-08-450-733-6
23	11.2	62.2	30	4	US-09-058-562-15
24	11.2	62.2	30	4	US-08-444-915A-6
25	11.2	62.2	30	5	PCT-US92-09752-15
26	11.2	62.2	34	1	US-08-411-795B-155
27	11.2	62.2	34	1	US-08-411-796-155

Sequence 155, App
Sequence 155, App
Sequence 155, App
Sequence 39, Appl
Sequence 39, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 80, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 2, Appl
Sequence 12, Appl
Sequence 42, Appl
Sequence 15, Appl
Sequence 14, Appl

US-08-646-265A-40
Sequence 40, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-646-265A-40

ALIGNMENTS

RESULT 1

US-08-646-265A-40
Sequence 40, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-646-265A-40

Query Match 71.1%; Score 12.8; DB 4; Length 47;
Best Local Similarity 87.5%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gatagtgcgcgagca 18
||||| |||||||
Db 17 GATAGGATGCCGAGTA 32

RESULT 2

US-08-591-492-16
; Sequence 16, Application US/08591492
; Patent No. 5756086
; GENERAL INFORMATION:
; APPLICANT: McClelland, Alan
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Adenoviruses Having Modified
; TITLE OF INVENTION: Fiber Proteins
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,492
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,078
; FILING DATE: 13-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: PCR DNA primer
US-08-591-492-16

Query Match 67.8%; Score 12.2; DB 1; Length 37;
Best Local Similarity 82.4%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tgatagtgcgcgagca 18
||||| ||| |||||
Db 21 TGATATCATGACGAGCA 37

RESULT 3

US-09-253-396A-73/c
; Sequence 73, Application US/09253396A
; Patent No. 6205404
; GENERAL INFORMATION:
; APPLICANT: Genome Dynamics, Inc.
; TITLE OF INVENTION: DNA-Binding Proteins of the Zinc-Finger Class
; FILE REFERENCE: 1116242-0003 file: genome03f.app

; CURRENT APPLICATION NUMBER: US/09/253,396A
; CURRENT FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-253-396A-73

Query Match 66.7%; Score 12; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 gtatgcgcgagca 18
||||| |||||||
Db 14 GTATGCCGAGCA 3

RESULT 4

US-09-235-246-16
; Sequence 16, Application US/09235246A
; Patent No. 6048719
; GENERAL INFORMATION:
; APPLICANT: Kong, Hulmin
; APPLICANT: Higgins, Lauren S.
; APPLICANT: Dalton, Michael A.
; TITLE OF INVENTION: Method For Cloning And Producing The DraIII Restriction
; TITLE OF INVENTION: Endonuclease
; FILE REFERENCE: DraIII
; CURRENT APPLICATION NUMBER: US/09/235,246A
; CURRENT FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Deinococcus radiophilus
US-09-235-246-16

Query Match 65.6%; Score 11.8; DB 3; Length 46;
Best Local Similarity 86.7%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtgatgtatgcgcgca 15
||||| ||||| |||
Db 19 gtgatgtatgcgcgca 33

RESULT 5

US-08-604-965E-14/c
; Sequence 14, Application US/08604965E
; Patent No. 6046033
; GENERAL INFORMATION:
; APPLICANT: Goto, Masaaki
; APPLICANT: Tsuda, Eisuke
; APPLICANT: Yano, Kazuki
; APPLICANT: Kobayashi, Fumie
; APPLICANT: Yamaguchi, Kyoji
; APPLICANT: Washida, Naohiro
; APPLICANT: Satake, Toshiko
; APPLICANT: Morinaga, Tomonori
; APPLICANT: Ueda, Masatsugu
; APPLICANT: Higashio, Kanji
; TITLE OF INVENTION: Basic Osteoblast Growth FactorII (bOGF-
; TITLE OF INVENTION: II)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burgess, Ryan and Wayne
; STREET: 370 Lexington Avenue, Suite 2105
; CITY: NEW YORK

STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,965E
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01270
FILING DATE: June 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milton J.
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-5212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-683-8150
TELEFAX: 212-532-4285
TELEX: 423794
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-604-965E-14

Query Match 63.3%; Score 11.4; DB 3; Length 26;
Best Local Similarity 92.3%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 agtatgccgagca 18
||||| |||||
Db 26 AGTATGCAGACGA 14

RESULT 6
US-08-604-965E-20/c
Sequence 20, Application US/08604965E
Patent No. 6046033
GENERAL INFORMATION:
APPLICANT: Goto, Masaaki
APPLICANT: Tsuda, Eisuke
APPLICANT: Yano, Kazuki
APPLICANT: Kobayashi, Fumie
APPLICANT: Yamaguchi, Kyoji
APPLICANT: Washida, Naohiro
APPLICANT: Satake, Toshiko
APPLICANT: Morinaga, Tomonori
APPLICANT: Ueda, Masatsugu
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Basic Osteoblast Growth Factor II (BOGF-II)
TITLE OF INVENTION: II)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burgess, Ryan and Wayne
STREET: 370 Lexington Avenue, Suite 2105
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/604,965E
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01270
FILING DATE: June 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milton J.
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-5212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-683-8150
TELEFAX: 212-532-4285
TELEX: 423794
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-604-965E-20

Query Match 63.3%; Score 11.4; DB 3; Length 26;
Best Local Similarity 92.3%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 agtatgccgagca 18
||||| |||||
Db 26 AGTATGCAGACGA 14

RESULT 7
US-08-724-354D-11
Sequence 11, Application US/08724354D
Patent No. 5994119
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-724-354D-11

Query Match 62.2%; Score 11.2; DB 2; Length 21;
Best Local Similarity 81.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tgatagtgcgcgagc 17
||| || ||| ||| |||
Db 4 TGACAGGATGCAGAGC 19

RESULT 8

US-09-270-984A-11
; Sequence 11, Application US/09270984A
; Patent No. 6048965
; GENERAL INFORMATION:
; APPLICANT: Dietz, Harry C.
; TITLE OF INVENTION: MAMMALIAN REGULATOR OF
; TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,984A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/724,354
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-270-984A-11

Query Match 62.2%; Score 11.2; DB 3; Length 21;
Best Local Similarity 81.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tgatagtgcgcgagc 17
||| || ||| ||| |||
Db 4 TGACAGGATGCAGAGC 19

RESULT 9

US-08-244-494A-1/c
; Sequence 1, Application US/08244494A
; Patent No. 5561114
; GENERAL INFORMATION:
; APPLICANT: KOMAI, Takahashi
; APPLICANT: MIYASHITA, Keiichi
; APPLICANT: SAKASHITA, Elji
; APPLICANT: KAMOGAWA, Hiroshi

; APPLICANT: INOUE, Fujio
; APPLICANT: TAKENISHI, Soichiro
; TITLE OF INVENTION: AN ADSORBENT FOR CELLULAR
; TITLE OF INVENTION: FIBRONECTIN, A METHOD FOR FRACTIONAL
; TITLE OF INVENTION: PURIFICATION OF FIBRONECTIN AND A
; TITLE OF INVENTION: METHOD OF HEMOCATHARSIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,494A
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 255199/1992
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGART, WADDELL A.
; REGISTRATION NUMBER: 24,861
; REFERENCE/DOCKET NUMBER: 035327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-244-494A-1

Query Match 62.2%; Score 11.2; DB 1; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtgatatgtgcgcgag 16
||| || ||| ||| |||
Db 17 GTGATGGAATTCGAG 2

RESULT 10

US-08-119-231-1/c
; Sequence 1, Application US/08119231
; Patent No. 5571679
; GENERAL INFORMATION:
; APPLICANT: SEKIGUCHI, KIYOTOSHI
; APPLICANT: ASAKAWA, KANEJI
; APPLICANT: SAKASHITA, ELJI
; APPLICANT: HINO, KAZUO
; APPLICANT: SHIN, SADAHIRO
; APPLICANT: TACHIKAWA, TETSUYA
; APPLICANT: HIRANO, HISANOBU
; TITLE OF INVENTION: ANTI-EDA MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 PENNSYLVANIA AVE., NW
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/119,231
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 61524/1991
; FILING DATE: 26-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 157966/1991
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 286668/1991
; FILING DATE: 31-OCT-1991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-7060
; TELEFAX: 202-293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-119-231-1

Query Match 62.2%; Score 11.2; DB 1; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtgatgtatgcccag 16
||||| ||| |||||
DB 17 GTGATGAATCCGAG 2

RESULT 11
US-08-628-343-1/c
; Sequence 1, Application US/08628343
; Patent No. 5734025
; GENERAL INFORMATION:
; APPLICANT: KOMAI, Takahashi
; APPLICANT: MIYASHITA, Keiichi
; APPLICANT: SAKASHITA, Eiichi
; APPLICANT: KAMOGAWA, Hiroshi
; APPLICANT: INOUE, Fujio
; APPLICANT: TAKENISHI, Soichiro
; TITLE OF INVENTION: AN ADSORBENT FOR CELLULAR
; TITLE OF INVENTION: FIBRONECTIN, A METHOD FOR FRACTIONAL
; TITLE OF INVENTION: PURIFICATION OF FIBRONECTIN AND A
; TITLE OF INVENTION: METHOD OF HEMOCATHARSIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,343
; FILING DATE: 05-APR-1996
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 255199/1992
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: PCT/JP93/01366
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: 08/244,494
; FILING DATE: 25-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGART, WADDELL, A.
; REGISTRATION NUMBER: 24,861
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-628-343-1

Query Match 62.2%; Score 11.2; DB 1; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtgatgtatgcccag 16
||||| ||| |||||
DB 17 GTGATGAATCCGAG 2

RESULT 12
US-08-448-204-26
; Sequence 26, Application US/08448204
; Patent No. 5593836
; GENERAL INFORMATION:
; APPLICANT: Niemiec, John
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detecting
; TITLE OF INVENTION: Pneumocystis carinii
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,204
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,089
; FILING DATE: 14-MAY-1993
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-08-448-204-26

Query Match 62.2%; Score 11.2; DB 1; Length 25;
Best Local Similarity 81.2%; Pred. No. 7.7e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tgatgtatgccgagc 17
||||| ||||| |||
Db 2 TCATAAGATGCCGAGC 17

RESULT 13

US-08-207-481-13
Sequence 13, Application US/08207481

Patent No. 5820866

GENERAL INFORMATION:

APPLICANT: Kappler, John W.

APPLICANT: Marrack, Philippa

TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL

TITLE OF INVENTION: REGULATION

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: SHERIDAN ROSS & MCINTOSH

STREET: 1700 LINCOLN STREET, SUITE 3500

CITY: DENVER

STATE: COLORADO

COUNTRY: USA

ZIP: 80202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/207,481

FILING DATE: 04-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kovarik, Joseph E.

REGISTRATION NUMBER: 33,005

REFERENCE/DOCKET NUMBER: 2879-8

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303/863-9700

TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-207-481-13

Query Match 62.2%; Score 11.2; DB 1; Length 27;

Best Local Similarity 81.2%; Pred. No. 7.8e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gatagtatgccgagca 18
||| ||| ||||| |||
Db 6 GAGAGGATGCCGTGCA 21

RESULT 14

PCT-US95-02689-13

Sequence 13, Application PC/TUS9502689

GENERAL INFORMATION:

APPLICANT: National Jewish Center for Immunology and

APPLICANT: Respiratory Medicine

APPLICANT: Kappler, John W.

APPLICANT: Marrack, Philippa

TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL REGULATION

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: SHERIDAN ROSS & MCINTOSH

STREET: 1700 LINCOLN STREET, SUITE 3500

CITY: DENVER

STATE: COLORADO
COUNTRY: USA
ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02689
FILING DATE: 03-MAR-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kovarik, Joseph E.

REGISTRATION NUMBER: 33,005

REFERENCE/DOCKET NUMBER: 2879-8-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303/863-9700

TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

PCT-US95-02689-13

Query Match 62.2%; Score 11.2; DB 5; Length 27;

Best Local Similarity 81.2%; Pred. No. 7.8e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gatagtatgccgagca 18
||| ||| ||||| |||
Db 6 GAGAGGATGCCGTGCA 21

RESULT 15

US-07-789-179-6

Sequence 6, Application US/07789179

Patent No. 5545727

GENERAL INFORMATION:

APPLICANT: HOFFMAN, STEPHEN J.

APPLICANT: LOOKER, DOUGLAS L.

APPLICANT: ROSENDAHL, MARY S.

APPLICANT: STETLER, GARY L.

APPLICANT: WAGENBACH, MICHAEL

APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATHEWS, ANTONY J.

TITLE OF INVENTION: PRODUCTION AND USE OF HEMOGLOBIN AND

TITLE OF INVENTION: ANALOGUES THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 SEVENTH STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/789,179

FILING DATE: 19911108

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/671,707

FILING DATE: 01-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/374,161
FILING DATE: 30-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/379,116
FILING DATE: 13-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/349,623
FILING DATE: 10-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HOFFMAN-5B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-789-179-6

Query Match 62.2%; Score 11.2; DB 1; Length 30;
Best Local Similarity 81.2%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tgatagtatgccgagc 17
|||||
Db 12 TGATTGCATGCCGAAC 27

Search completed: October 12, 2002, 16:54:36
Job time: 8991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:29 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: us-09-945-131-3

Perfect score: 18

Sequence: 1 gtgatagtagtcgcgagca 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pna/US06_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US080_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US081_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US082_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US083_COMB.seq.*
- 8: /cgn2_6/ptodata/2/pna/US084_COMB.seq.*
- 9: /cgn2_6/ptodata/2/pna/US085_COMB.seq.*
- 10: /cgn2_6/ptodata/2/pna/US086_COMB.seq.*
- 11: /cgn2_6/ptodata/2/pna/US087_COMB.seq.*
- 12: /cgn2_6/ptodata/2/pna/US088_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	18	16	US-09-241-561-3	Sequence 3, Appli
2	14.4	80.0	25	62	US-60-234-049-123602	Sequence 123602,
3	13.4	74.4	25	35	US-09-954-427-357122	Sequence 357122,
4	13.4	74.4	25	35	US-09-954-427-357123	Sequence 357123,
5	13.4	74.4	25	35	US-09-954-427-357134	Sequence 357134,
6	13.4	74.4	25	35	US-09-954-429A-14687	Sequence 14687, A
7	13.4	74.4	25	35	US-09-954-429A-14688	Sequence 14688, A
8	13.4	74.4	25	35	US-09-954-429A-14689	Sequence 14689, A
9	13.4	74.4	25	35	US-09-956-584-141745	Sequence 141745,
10	13.4	74.4	25	62	US-60-233-166-357122	Sequence 357122,
11	13.4	74.4	25	62	US-60-233-166-357123	Sequence 357123,
12	13.4	74.4	25	62	US-60-233-166-357134	Sequence 357134,
13	13.4	74.4	25	62	US-60-233-357-17436	Sequence 17436, A
14	13.4	74.4	25	62	US-60-233-357-17437	Sequence 17437, A
15	13.4	74.4	25	62	US-60-233-357-17438	Sequence 17438, A
16	13.4	74.4	25	62	US-60-233-620-84925	Sequence 84925, A
17	13.4	74.4	25	62	US-60-233-620-84926	Sequence 84926, A
18	13.4	74.4	25	62	US-60-234-017-132654	Sequence 132654,
19	13.4	74.4	25	74	US-60-353-987-305023	Sequence 305023,
20	13.2	73.3	47	60	US-60-216-745-1570	Sequence 1570, Ap
21	13.2	73.3	50	29	US-09-755-374A-11926	Sequence 11926, A
22	13	72.2	25	74	US-60-353-987-53045	Sequence 53045,
23	12.8	71.1	25	35	US-09-954-427-180775	Sequence 180775,
24	12.8	71.1	25	35	US-09-954-427-306269	Sequence 306269,
25	12.8	71.1	25	35	US-09-956-584-278693	Sequence 278693,
26	12.8	71.1	25	62	US-60-233-166-180775	Sequence 180775,
27	12.8	71.1	25	62	US-60-233-166-306269	Sequence 306269,
28	12.8	71.1	25	62	US-60-234-017-266246	Sequence 266246,
29	12.8	71.1	25	74	US-60-353-987-916688	Sequence 916688,
30	12.8	71.1	47	26	US-09-671-317-523	Sequence 523, App
31	12.8	71.1	47	29	US-09-749-873-40	Sequence 40, Appl

Sequence 357124, A
Sequence 357125, A
Sequence 14686, A
Sequence 14690, A
Sequence 22741, A
Sequence 574177, A
Sequence 574187, A
Sequence 357124, A
Sequence 357125, A
Sequence 17435, A
Sequence 17439, A
Sequence 106965, A
Sequence 42411, A
Sequence 575065, A

32	12.4	68.9	25	35	US-09-95A-427-357125
33	12.4	68.9	25	35	US-09-95A-427-357125
34	12.4	68.9	25	35	US-09-95A-429A-146866
35	12.4	68.9	25	35	US-09-95A-429A-146900
36	12.4	68.9	25	35	US-09-956-584-22741
37	12.4	68.9	25	35	US-09-956-584-574177
38	12.4	68.9	25	35	US-09-956-584-574187
39	12.4	68.9	25	62	US-60-233-166-357124
40	12.4	68.9	25	62	US-60-233-166-357125
41	12.4	68.9	25	62	US-60-233-357-17435
42	12.4	68.9	25	62	US-60-233-357-17439
43	12.4	68.9	25	62	US-60-233-620-106965
44	12.4	68.9	25	62	US-60-234-017-42411
45	12.4	68.9	25	62	US-60-234-017-575065

ALIGNMENTS

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RESULT      1
US-09-241-561-3
; Sequence 3, Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-3

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Query Match      100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 gtgatagtatgccgagca 18
|||||
Db 1 gtqatagtatgccgagca 18

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RESULT      2
US-60-234-049-123602
; Sequence 123602, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Escherichia coli
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123602
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
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; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: GenBank U00096
 US-60-234-049-123602

Query Match	80.0%;	Score 14.4;	DB 62;	Length 25;
Best Local Similarity	93.8%;			
Pred. No. 5e+02;				
Matches 15;	Conservative	0;	Mismatches	1;
Indels				
Qy	1	gtgatagtagtcgcgag	16	
Db	8	qtgatagtagtcgcgag	23	

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RESULT      3
US-09-954-427-357122
: Sequence 357122, Application US/09954427
: GENERAL INFORMATION:
: APPLICANT: Mittmann
: APPLICANT: Affymetrix, Inc.
: TITLE OF INVENTION: Methods of Genetic Ana-
: TITLE OF INVENTION: Genome
: FILE REFERENCE: 3112
: CURRENT APPLICATION NUMBER: US/09/954,427
: CURRENT FILING DATE: 2001-09-17
: NUMBER OF SEQ ID NOS: 420907
: SOFTWARE: fastseq for Windows version 4.0
: SEQ ID NO 357122
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: GenBank U77777
US-09-954-427-357122

```

Query Match 74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14: Conservative 0; Mismatches 1; Indels

Qy 4 atagtatgccgagca 18
 ||||| |||||
 Db 10 atagtattccgagca 24

```

RESULT# 4
US-09-954-427-357123
; Sequence 357123, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Ana
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357123
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-09-954-427-357123

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```

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.le=03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtatgccagca 18
        ||||| |||||

```



```
Db      8 atagtattccgagca 22

RESULT 5
; Sequence 357134, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE OF INVENTION: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-09-954-427-357134

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
        ||||||| |||||||
Db      6 atagtattccgagca 20

RESULT 6
US-09-954-429A-14687
; Sequence 14687, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE OF INVENTION: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 14687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429A-14689

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
        ||||||| |||||||
Db      6 atagtattccgagca 20

RESULT 7
US-09-954-429A-14688
; Sequence 14688, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE OF INVENTION: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 14687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429A-14687

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
        ||||||| |||||||
Db      6 atagtattccgagca 20

RESULT 8
US-09-954-429A-14689
; Sequence 14689, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE OF INVENTION: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 14689
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429A-14689

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
        ||||||| |||||||
Db      8 atagtattccgagca 22

RESULT 9
US-09-956-584-141745
; Sequence 141745, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE OF INVENTION: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-141745

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
        ||||||| |||||||
Db      10 atagtattccgagca 24

RESULT 9
US-09-956-584-141745
; Sequence 141745, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE OF INVENTION: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-141745

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
```

APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat

LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-357-17437

Query Match 74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 atagtattccgagca 18
| | | | | | | | | |
Db 8 atagtattccgagca 22

RESULT 15
US-60-233-357-17438
; Sequence 17438, Application US/60233357
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; TITLE OF INVENTION: Neurobiology
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-357-17438

Query Match 74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 atagtattccgagca 18
| | | | | | | | | |
Db 6 atagtattccgagca 20

Search completed: October 12, 2002, 20:42:30
Job time: 16400 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:28 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-3
Perfect score: 18
Sequence: 1 gtgatagatgccgagca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New : *
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq : *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq : *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq : *
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq : *
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq : *
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq : *
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq : *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-3
2	14.4	80.0	25	5	US-09-956-604-109679
3	12.2	67.8	25	5	US-09-396-196G-59455
4	12.2	67.8	25	5	US-09-396-196G-59456
5	12.2	67.8	25	5	US-09-396-196G-107073
6	11.8	65.6	16	1	PCT-US02-25943-62317
7	11.8	65.6	17	1	PCT-US02-25943-62319
8	11.8	65.6	18	1	PCT-US02-11683-26
9	11.8	65.6	18	7	US-10-122-013-26
10	11.8	65.6	23	5	US-09-803-876A-17
11	11.8	65.6	40	6	US-10-035-832-607
12	11.8	65.6	40	7	US-10-105-613-147
13	11.8	65.6	42	7	US-10-170-097-756
14	11.6	64.4	25	5	US-09-956-604-18296
15	11.4	63.3	15	1	PCT-US02-25940-6508
16	11.4	63.3	15	1	PCT-US02-25940-11096
17	11.4	63.3	17	1	PCT-US02-25943-32518
18	11.4	63.3	17	1	PCT-US02-25943-55833
19	11.4	63.3	18	1	PCT-US02-25940-129
20	11.4	63.3	20	1	PCT-US02-25940-6507
21	11.4	63.3	20	1	PCT-US02-25940-6509
22	11.4	63.3	22	1	PCT-US02-25943-52885
23	11.4	63.3	23	1	PCT-US02-25943-13010
24	11.4	63.3	25	5	US-09-956-604-129261
25	11.4	63.3	25	5	US-09-396-196G-3199

c 26	11.4	63.3	25	5	US-09-396-196G-3200	Sequence 3200, Ap
c 27	11.4	63.3	25	5	US-09-396-196G-84295	Sequence 84295, A
c 28	11.4	63.3	25	5	US-09-396-196G-84296	Sequence 84296, A
c 29	11.4	63.3	25	5	US-09-396-196G-84297	Sequence 84297, A
c 30	11.4	63.3	32	1	PCT-US02-25940-14492	Sequence 14492, A
c 31	11.4	63.3	34	1	PCT-US02-25943-33116	Sequence 33116, A
c 32	11.4	63.3	39	1	PCT-US02-25943-33117	Sequence 33117, A
c 33	11.2	62.2	20	7	US-10-128-560-85	Sequence 85, Appl
c 34	11.2	62.2	20	7	US-10-128-560-185	Sequence 185, Appl
c 35	11.2	62.2	25	5	US-09-956-604-95770	Sequence 95770, A
c 36	11.2	62.2	25	5	US-09-956-604-108981	Sequence 108981, A
c 37	11.2	62.2	25	5	US-09-956-604-113654	Sequence 113654, A
c 38	11.2	62.2	25	5	US-09-956-604-128604	Sequence 128604, A
c 39	11.2	62.2	25	5	US-09-396-196G-45766	Sequence 45766, A
c 40	11.2	62.2	25	5	US-09-396-196G-45767	Sequence 45767, A
c 41	11.2	62.2	25	6	US-10-215-112-12832	Sequence 12832, A
c 42	11.2	62.2	26	1	PCT-US02-25943-38378	Sequence 38378, A
c 43	11.2	62.2	34	7	US-10-078-113-155	Sequence 155, App
c 44	11.2	62.2	34	7	US-10-090-182A-155	Sequence 155, App
c 45	11.2	62.2	34	7	US-10-179-940-155	Sequence 155, App

ALIGNMENTS

RESULT 1
US-09-945-131-3
; Sequence 3, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-3

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.64; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgatagatgccgagca 18
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Db 1 gtgatagatgccgagca 18

RESULT 2
US-09-956-604-109679
; Sequence 109679, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19

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; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 109679
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-109679
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Query Match      80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 gtgatagtatgccgag 16
    ||||| ||||| |||||
DB 8 gtgatagtaagccgag 23
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```
RESULT 3
US-09-396-196G-59455/c
; Sequence 59455, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-59455
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```
Query Match      67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 gtgatagtatgccgag 17
    ||||| ||||| |||||
DB 24 GTGAGGATATGCCGAGC 8
```

```
RESULT 4
US-09-396-196G-59456/c
; Sequence 59456, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-59456
```

```
Query Match      67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 gtgatagtatgccgag 17
    ||||| ||||| |||||
DB 21 GTGAGGATATGCCGAGC 5
```

```
RESULT 5
US-09-396-196G-107073/c
; Sequence 107073, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107073
```

```
Query Match      67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 gtgatagtatgccgag 17
    ||||| ||||| |||||
DB 20 GTAATAGTAGTGGGAGC 4
```

```
RESULT 6
PCT-US02-25943-62317/c
; Sequence 62317, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62317
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6082328)...(6082343)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 66
PCT-US02-25943-62317
```

```
Query Match      65.6%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 atagtatgccgagca 18
    ||||| ||||| |||||
DB 16 AGAGCATATGCCGAGCA 2
```

```
RESULT 7
PCT-US02-25943-32519/c
; Sequence 32519, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jlm Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 32519
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3178057)...(3178073)
; OTHER INFORMATION: Chromosome - 1 Strand = positive ConnectronObjectNumber = 34846
PCT-US02-25943-32519

Query Match 65.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 atagtatgccgagca 18
| | | | | | | | | | | | | | | | | |
Db 17 AGAGCATGCCGACCA 3

RESULT 8
PCT-US02-11683-26/c
; Sequence 26, Application PC/TUS0211683
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK ET AL
; TITLE OF INVENTION: NUCLEIC ACIDS FOR INHIBITING HAIRLESS PROTEIN EXPRESSION AND METH
; FILE REFERENCE: USE THEREOF
; CURRENT APPLICATION NUMBER: PCT/US02/11683
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIALSEQUENCE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: ANTISENSEOLIGONUCLEOTIDEDIRECTED AT HUMAN HAIRLESS
PCT-US02-11683-26

Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gatagtatgccgagc 17
| | | | | | | | | | | | | | | | | |
Db 15 GAGAGTATGCCGACG 1

RESULT 9
US-10-122-013-26/c
; Sequence 26, Application US/10122013
; GENERAL INFORMATION:
; APPLICANT: Christiano, Angela
; TITLE OF INVENTION: NUCLEIC ACIDS FOR INHIBITING HAIRLESS PROTEIN EXPRESSION AND METH
; FILE REFERENCE: USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/122,013
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIALSEQUENCE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: ANTISENSEOLIGONUCLEOTIDEDIRECTED AT HUMAN HAIRLESS
US-10-122-013-26

Query Match 65.6%; Score 11.8; DB 7; Length 18;
Best Local Similarity 86.7%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gatagtatgccgagc 17
| | | | | | | | | | | | | | | | | |
Db 15 GAGAGTATGCCGACG 1

RESULT 10
US-09-803-676A-17
; Sequence 17, Application US/09803676A
; GENERAL INFORMATION:
; APPLICANT: Terry, L. I.
; APPLICANT: Chase, Kevin
; TITLE OF INVENTION: QUANTITATIVE TRAIT LOCI FOR INSECT RESISTANCE IN PLANTS
; FILE REFERENCE: 14-00
; CURRENT APPLICATION NUMBER: US/09/803,676A
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,439
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 17
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide Primer
US-09-803-676A-17

Query Match 65.6%; Score 11.8; DB 5; Length 23;
Best Local Similarity 86.7%; Pred. No. 3.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtgatatgtatgccga 15
| | | | | | | | | | | | | | | | | |
Db 2 gtgacagtataccga 16

RESULT 11
US-10-035-832-607
; Sequence 607, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 607
; LENGTH: 40
; TYPE: DNA
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; ORGANISM: Mus musculus
US-10-035-832-607

Query Match 65.6%; Score 11.8; DB 6; Length 40;
Best Local Similarity 86.7%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 gatagtagccgagc 17
||||| |||||
Db 13 gatagtaagccggc 27

RESULT 12
US-10-105-613-147
; Sequence 147, Application US/10105613
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER
; FILE REFERENCE: A-69959/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/105,613
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US/09/747,377
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 493
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-105-613-147

Query Match 65.6%; Score 11.8; DB 7; Length 40;
Best Local Similarity 86.7%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 gatagtagccgagc 17
||||| |||||
Db 13 gatagtaagccggc 27

RESULT 13
US-10-170-097-756
; Sequence 756, Application US/10170097
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GEN-T114XC2d1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 756
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele

; LOCATION: 24
; OTHER INFORMATION: 12-389-431 : polymorphic base C or T
US-10-170-097-756

Query Match 65.8%; Score 11.8; DB 7; Length 42;
Best Local Similarity 76.5%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 gtgatagtatgccgagc 17
|:|:| ||||| |||||
Db 23 gygaaagtatgttgagc 39

RESULT 14
US-09-956-604-18296/c
; Sequence 18296, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-18296

Query Match 64.4%; Score 11.6; DB 5; Length 25;
Best Local Similarity 77.8%; Pred. No. 5.1e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 gtgatagtatgccgagca 18
| | ||||| |||||
Db 18 GGTCTAGTAGCCGAGCA 1

RESULT 15
PCT-US02-25940-6508
; Sequence 6508, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 6508
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (807312)...(807326)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 7
PCT-US02-25940-6508

Query Match 63.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 agtatgccgagca 18
|| ||||| |||||
Db 1 aggatgccgagca 13

Search completed: October 12, 2002, 17:27:29
Job time: 10804 sec

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Query Match      72.2%; Score 13; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagga 18
|||||
Db 31 CGTAAGCCTAGGA 19

RESULT 2
AX078109/c
LOCUS AX078109 33 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 3 from Patent WO0106016.
ACCESSION AX078109
VERSION AX078109.1 GI:13157854
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 33)
AUTHORS
TITLE Amplification of nucleic acids with electronic detection
JOURNAL Patent: WO 0106016-A 3 25-JAN-2001;
Clinical Micro Sensors, Inc. (US)
FEATURES
source
1..33
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic."
BASE COUNT 6 a 11 c 8 g 8 t
ORIGIN

Query Match      72.2%; Score 13; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagga 18
|||||
Db 31 CGTAAGCCTAGGA 19

RESULT 3
ARI63935/c
LOCUS ARI63935 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 133 from patent US 6271030.
ACCESSION ARI63935
VERSION ARI63935.1 GI:16234779
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 133 07-AUG-2001;
FEATURES
source
1..20
/organism="unknown"
BASE COUNT 4 a 7 c 6 g 3 t
ORIGIN

Query Match      71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 7.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gttacgtaacgctagg 17
|||||
Db 17 GTTAGTGAGCCTCGG 2

Query Match      72.2%; Score 13; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagga 18
|||||
Db 31 CGTAAGCCTAGGA 19

RESULT 4
AX0839
LOCUS AX0839 34 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 6 from Patent WO9810083.
ACCESSION AX0839
VERSION AX0839.1 GI:4774842
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Meredith,D.M. and Markham,A.F.
TITLE HERPESVIRUS SAIMIRI AS VIRAL VECTOR
JOURNAL Patent: WO 9810083-A 6 12-MAR-1998;
MEREDITH DAVID MARK (GB)
FEATURES
source
1..34
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 10 a 6 c 5 g 13 t
ORIGIN

Query Match      71.1%; Score 12.8; DB 6; Length 34;
Best Local Similarity 87.5%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ttacgtaacgctagga 18
|||||
Db 1 TTGCTTAAGCCTAGGA 16

RESULT 5
AX025105
LOCUS AX025105 34 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 6 from Patent WO0032802.
ACCESSION AX025105
VERSION AX025105.1 GI:10186887
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Meredith,D.M. and Markham,A.F.
TITLE Hiv vaccine
JOURNAL Patent: WO 0032802-A 6 08-JUN-2000;
MEREDITH DAVID MARK (GB); UNIV LEEDS (GB); MARKHAM ALEXANDER FRED (GB)
FEATURES
source
1..34
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="VIRAL PRIMER/ LINKER"
BASE COUNT 10 a 6 c 5 g 13 t
ORIGIN

Query Match      71.1%; Score 12.8; DB 6; Length 34;
Best Local Similarity 87.5%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ttacgtaacgctagga 18
|||||
Db 1 TTGCTTAAGCCTAGGA 16

RESULT 6
A70835
LOCUS A70835 18 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 2 from Patent WO9810083.
ACCESSION A70835
VERSION A70835.1 GI:4774838
KEYWORDS
```

JOURNAL	PATENT: US 5814517-A 112 29-SEP-1998;
FEATURES	Location/Qualifiers
SOURCE	1..18
BASE COUNT	4 a 4 c 4 g 6 t
ORIGIN	/organism="unknown"
Query Match	66.7%; Score 12; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 2.3e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 cggtacgtaagc 12
Db	17 CGTTACGTAAGC 6
RESULT	9
LOCUS	AR043743
DEFINITION	Sequence 113 from patent US 5814517.
ACCESSION	AR043743
VERSION	AR043743.1 GI:5964751
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Seidel,H.Martin., and Lamb,I.Peter.
TITLE	DNA spacer regulatory elements responsive to cytokines and methods for their use
JOURNAL	PATENT: US 5814517-A 113 29-SEP-1998;
FEATURES	Location/Qualifiers
SOURCE	1..18
BASE COUNT	6 a 4 c 4 g 4 t
ORIGIN	/organism="unknown"
Query Match	66.7%; Score 12; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 2.3e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 cggtacgtaagc 12
Db	6 CGTTACGTAAGC 17
RESULT	10
LOCUS	AR063624
DEFINITION	Sequence 35 from patent US 5846715.
ACCESSION	AR063624
VERSION	AR063624.1 GI:5992932
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 31)
AUTHORS	Purcell,D.Francis.John., Russell,S.May. and McKenzie,I.Farquar.Campbell.
TITLE	CD46 variants
JOURNAL	PATENT: US 5846715-A 35 08-DEC-1998;
FEATURES	Location/Qualifiers
SOURCE	1..31
BASE COUNT	9 a 6 c 7 g 9 t
ORIGIN	/organism="unknown"
Query Match	65.6%; Score 11.8; DB 6; Length 31;
Best Local Similarity	86.7%; Pred. No. 3e+04;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 4 tacgtaagccttagga 18
   || || || || || || || ||
Db 1 TAAGTAGGCCTAGGA 15

RESULT 11
A18606/c
LOCUS A18606 42 bp DNA linear PAT 26-JAN-1995
DEFINITION H. sapiens CD46 exon 9 (STP C).
ACCESSION A18606
VERSION A18606.1 GI:513317
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 42)
AUTHORS
TITLE CD46 VARIANTS
JOURNAL Patent: WO 9118097-A 25 28-NOV-1991;
FEATURES Location/Qualifiers
   source
       /organism="synthetic construct"
       /db_xref="taxon:32630"
       <1..42
       /note="H. sapiens CD46 exon 9 (STP C)"
       /number=9
BASE COUNT 11 a 14 c 6 g 11 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 42;
Best Local Similarity 86.7%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 tacgtaagccttagga 18
   || || || || || || || ||
Db 16 TAAGTAGGCCTAGGA 2

RESULT 12
AR063615/c
LOCUS AR063615 42 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5846715.
ACCESSION AR063615
VERSION AR063615.1 GI:5992923
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 42)
AUTHORS Purcell,D.Francis.John., Russell,S.May. and
        McKenzie,I.Farquar.Campbell.
TITLE CD46 variants
JOURNAL Patent: US 5846715-A 19 08-DEC-1998;
FEATURES Location/Qualifiers
   source
       /organism="unknown"
BASE COUNT 11 a 14 c 6 g 11 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 42;
Best Local Similarity 86.7%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 tacgtaagccttagga 18
   || || || || || || || ||
Db 16 TAAGTAGGCCTAGGA 2

RESULT 13
AX289339
LOCUS AX289339 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 1101 from Patent WO0179548.
ACCESSION AX289339
VERSION AX289339.1 GI:17051022
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (sites)
AUTHORS Barany,F., Zlrvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
        sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 1101 25-OCT-2001;
FEATURES Location/Qualifiers
   source
       /organism="synthetic construct"
       /db_xref="taxon:32630"
       /note="Hypothetical Probe Sequence"
BASE COUNT 5 a 8 c 5 g 6 t
ORIGIN
Query Match 64.4%; Score 11.6; DB 6; Length 24;
Best Local Similarity 77.8%; Pred. NO. 4.1e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttagga 18
   || || || || || || || ||
Db 1 CGTTACGGAATCCTTGCA 18

RESULT 14
ECORRG15
LOCUS ECORRG15 38 bp rRNA linear BCT 11-AUG-1995
DEFINITION E.coli 23S ribosomal RNA, fragment J.
ACCESSION K01121
VERSION K01121.1 GI:174396
KEYWORDS 23S ribosomal RNA; ribosomal RNA.
SEGMENT 15 of 26
SOURCE Escherichia coli rRNA.
ORGANISM Escherichia coli
REFERENCE 1 (bases 1 to 38)
AUTHORS Branlant,C., Krol,A., Machatt,M.A. and Ebel,J.P.
TITLE Structural study of ribosomal 23 S RNA from Escherichia coli
JOURNAL FEBS Lett. 107 (1), 177-181 (1979)
MEDLINE 80047286
COMMENT See segment 1.
FEATURES Location/Qualifiers
   source
       /organism="Escherichia coli"
       /db_xref="taxon:562"
       <1..38
       /product="23S ribosomal RNA"
BASE COUNT 6 a 4 c 17 g 11 t
ORIGIN
Query Match 64.4%; Score 11.6; DB 1; Length 38;
Best Local Similarity 77.8%; Pred. NO. 4.1e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttagga 18
   || || || || || || || ||
Db 18 CGTTCGTGAAGCCTGTGA 35

RESULT 15
E37995/c
LOCUS E37995 42 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing protein variant, process for constructing

```

protein variant library, and process for constructing protein variant-encoding cDNA library.

ACCESSION E37995
VERSION E37995.1 GI:18626896
KEYWORDS JP 2000236880-A/13.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 42)
AUTHORS Imamura,T., Asada,M., Suzuki,M., Oka,S. and Yoneda,A.
TITLE Process for producing protein variant, process for constructing protein variant library, and process for constructing protein variant-encoding cDNA library
JOURNAL Patent: JP 2000236880-A 13 05-SEP-2000;
COMMENT AGENCY OF IND SCIENCE & TECHNOL
OS Artificial Sequence
PN JP 2000236880-A/13
PD 05-SEP-2000
PF 19-FEB-1999 JP 1999041538
PR
PI TORU IMAMURA,MASAHIRO ASADA,MAKOTO SUZUKI,SHUICHI OKA, PI
ATSUOKO YONEDA
PC C12N15/09,C07K14/475,C12N5/10,C12P21/02//(C12N15/09,C12R1:91),
PC (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1..42 /organism='Artificial Sequence'.
1..42 Location/Qualifiers
/organism='synthetic construct'
/db_xref='taxon:32630'

BASE COUNT 9 a 16 c 7 g 10 t

Query Match 64.4%; Score 11.6; DB 6; Length 42;
Best Local Similarity 77.8%; Pred. No. 4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
||| ||||| |||
DB 25 CGTAACCTTAAGCCGGGA 8

Search completed: October 12, 2002, 16:51:16
Job time: 8891 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:02 ; Search time 792.17 seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-4

Perfect score: 18

Sequence: 1 cgttacgtaagcctagga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18	100.0	18	21	AAAI3835
2	13.2	73.3	26	16	AAQ89868
3	12.8	71.1	34	21	AAA60557
4	12.2	67.8	18	21	AAA60553
5	12.2	67.8	25	16	AAQ99545
6	12.2	67.8	38	21	AACT3635
7	12	66.7	18	19	AAV56953
8	12	66.7	18	19	AAV56954
9	11.8	65.6	31	12	AAQ14923

10	11.8	65.6	50	22	AAAL33677	Human SNP oligonucleotide
11	11.6	64.4	24	24	ABI84598	Capture oligonucleotide
12	11.6	64.4	24	24	ABI84599	Capture oligonucleotide
13	11.6	64.4	42	21	AAQ66117	PCR primer #3n-IR
14	11.6	64.4	50	17	AAQ35090	Oligonucleotide wh
15	11.6	64.4	50	17	AAAT41692	Oligonucleotide co
16	11.6	64.4	50	17	AAAT37107	Oligonucleotide ha
17	11.4	63.3	22	18	AAAT84535	Serotonin transpor
18	11.4	63.3	27	18	AAAT91263	GBV hepatitis viru
19	11.4	63.3	36	10	AAAN0552	Tissue plasminogen
20	11.4	63.3	47	18	AAAT74123	AACT-K391T/K396T d
21	11.2	62.2	20	22	AAAF59668	HBV surface antige
22	11.2	62.2	25	16	AAQ92995	Pre-invasive human
23	11.2	62.2	25	19	AAV19232	Primer ON6 to ampl
24	11.2	62.2	27	14	AAQ43337	Sequence of PCR pr
25	11.2	62.2	27	21	AAZ55159	Neisseria species
26	11.2	62.2	28	17	AAAT33625	Primer for murine
27	11.2	62.2	29	19	AAV44042	Mouse bFGF recepto
28	11.2	62.2	32	22	AAAT7813	CREB probe derived
29	11.2	62.2	34	17	AAAT31729	Escherichia coli c
30	11.2	62.2	35	14	AAQ43340	Sequence of PCR pr
31	11.2	62.2	37	19	AAV04084	Somatostatin gene
32	11.2	62.2	39	18	AAAT87127	IFN-gamma 2'F RNA
33	11.2	62.2	40	20	AAAX90938	Oligonucleotide cr
34	11.2	62.2	40	21	AAAX92339	Hepatitis B virus
35	11.2	62.2	44	20	AAAX90937	Oligonucleotide cr
36	11.2	62.2	45	22	AAAS09526	Human IL-17b hybri
37	11.2	62.2	47	19	AAV30386	Oligomer p47rg24 u
38	11.2	62.2	50	21	AAZ91705	P. microspora telo
39	11.2	62.2	50	21	AAZ91716	P. microspora telo
40	11.2	62.2	50	22	AAAT74731	Human silent SNP c
41	11.2	62.2	50	22	AAAT74733	Human silent SNP c
42	11	61.1	20	20	AAZ02278	PCR primer used to
43	11	61.1	27	22	AAAS09842	Primer for detecti
44	11	61.1	30	17	AAAT33118	Primer 2A for ampl
45	10.8	60.0	16	18	AAAT92448	TAT system oligonu

ALIGNMENTS

RESULT	1
AAAI3835	
ID	AAAI3835 standard; DNA; 18 BP.
AC	AAAI3835;
XX	
XX	27-JUL-2000 (first entry)
DT	
DE	Murine PDGFR-beta scrambled control oligonucleotide SEQ ID NO:4.
XX	
XX	Murine; mouse; platelet derived growth factor receptor beta; vasotropic; PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis; recurrent stenosis; cardiovascular injury; ss.
KW	
KW	
XX	
OS	Mus sp.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1..18
FT	/*tag= a
XX	/note= "phosphorothioate linkages"
PN	CA2228977-A1.
XX	
PD	07-MAY-1999.
XX	
PF	03-FEB-1998; 98CA-2228977.
XX	
PR	07-NOV-1997; 97CA-2215360.
XX	
PA	(EDEL/) EDELMAN E R.
PA	(ROSE/) ROSENBERG R D.
PA	(SIRO/) SIROIS M G.

PA (SIMO/) SIMONS M.
 XX
 XX Edelman ER, Rosenberg RD, Sirois MG, Simons M;
 XX WPI; 2000-283933/25.
 XX
 XX Antisense inhibition of platelet derived growth factor beta-receptor
 PT subunit expression for the prevention of restenosis -
 PT
 XX Example 1; Page 15; 43pp; English.
 XX
 XX A method has been developed for preventing restenosis following vascular
 CC injury by antisense inhibition of platelet derived growth factor
 CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
 CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
 CC canal), especially of a valve in the heart, after surgical correction of
 CC the primary condition) following cardiovascular injury. The present
 CC sequence represents a scrambled control phosphorothioate oligonucleotide
 CC for murine PDGFR-beta, which is used in an example from the present
 CC invention.
 XX
 XX Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
 |||||
 Db 1 cgttacgtaagcctagga 18

RESULT 2
 AAQ89868
 ID AAQ89868 standard; DNA; 26 BP.
 XX
 XX AAQ89868;
 DT 02-JAN-1996 (first entry)
 XX
 XX SV40 1093 PCR primer for generating nucleic acid marker ladder.
 DE
 XX Nucleic acid marker ladder; DNA; gel electrophoresis; PCR; primer;
 KW ss.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH misc_feature 1
 FT /*tag= a
 FT /note= "10 nucleotide spacer is present, 5' to
 FT guanine at position 1"
 FT
 FT misc_feature 1..6
 FT /*tag= b
 FT /function= BamHI_restriction_site
 FT 7..26
 FT /*tag= c
 FT /note= "Anneals to DNA template"
 FT
 XX W09511971-A1.
 PN
 XX
 XX 04-MAY-1995.
 PD
 XX
 XX 28-OCT-1994; 94WO-US12505.
 PF
 XX
 XX 28-OCT-1993; 93US-0142124.
 PR
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 PA
 XX Hartley JL;
 PI
 XX WPI; 1995-178864/23.
 DR

XX
 PT Nucleic acid (NA) marker ladder for estimating mass of NA mol. -
 PT comprises at least 3 fragments from complete restriction
 PT endonuclease digestion, with fragment lengths being multiples of an
 PT integer
 XX
 XX Example 2; Page 12; 22pp; English.
 XX
 XX The primers AAQ89865-Q89870 are PCR primers used in the construction
 CC of a new NotI marker ladder. Each primer consists of a spacer sequence,
 CC an area of annealing DNA, and one or more restriction sites. The spacing
 CC of the priming sites and the restriction sites is such that when the
 CC three PCR products are annealed together to form a circular molecule,
 CC the resulting 3500bp plasmids can be cleaved with NotI to give three
 CC fragments of 2000, 1000 and 500bp. The marker ladder is useful as a
 CC standard for determining the mass of nucleic acid molecules during gel
 CC electrophoresis.
 XX
 XX Sequence 26 BP; 6 A; 4 C; 11 G; 5 T; 0 other;
 SQ

Query Match 73.3%; Score 13.2; DB 16; Length 26;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
 |||||
 Db 6 cgtgaggtgagcctagga 23

RESULT 3
 AAA60557
 ID AAA60557 standard; DNA; 34 BP.
 XX
 XX AAA60557;
 AC
 XX 20-OCT-2000 (first entry)
 DT
 XX
 XX Recombination cassette pMSL104 construction oligomer SEQ ID NO:6.
 DE
 XX HIV; vaccine; herpesvirus saimiri; HVS; envelope protein; anti-HIV;
 KW Immune response; ss.
 KW
 XX Synthetic.
 OS
 XX W0200032802-A1.
 PN
 XX 08-JUN-2000.
 PD
 XX
 XX 25-NOV-1999; 99WO-GH03923.
 PF
 XX
 XX 28-NOV-1998; 98GB-0026069.
 PR
 XX (UYLE-) UNIV LEEDS.
 PA
 XX Meredith DM, Markham AF;
 PI
 XX WPI; 2000-412347/35.
 DR
 XX Herpesvirus saimiri vector comprising a gene encoding an envelope
 PT protein of human immunodeficiency virus (HIV), useful as a vaccine for
 PT treating HIV infection and for delivering the protein to a specific
 PT cell population -
 PT
 XX Disclosure; Page 17; 33pp; English.
 PS
 XX The present invention describes a herpesvirus saimiri (HVS) vector (I),
 CC having part of a gene encoding an envelope protein of human
 CC immunodeficiency virus (HIV), for delivering the protein to a specific
 CC cell population. (I) is useful as a vaccine for inducing a humoral
 CC and/or cellular anti-protein immune response to a T lymphocyte or
 CC macrophage population, for manufacturing medicaments for preventing
 CC and/or treating an individual likely to contract or suffering from HIV

CC infection, and for delivering selected HIV heterogeneous genetic
CC material to a specific cell population. The present sequence represents
CC an oligonucleotide which is used in the exemplification of the present
CC invention.

SQ Sequence 34 BP; 10 A; 6 C; 5 G; 13 T; 0 other;

Query Match 71.1%; Score 12.8; DB 21; Length 34;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ttacgtaagcctagga 18
||| |||||

DB 1 ttgcttaagcctagga 16
||| |||||

RESULT 4
AAA60553
ID AAA60553 standard; DNA; 18 BP.

XX AC AAA60553;

XX 20-OCT-2000 (first entry)

XX Recombination cassette pMSL102 construction oligomer SEQ ID NO:2.
XX HIV; vaccine; herpesvirus saimiri; HVS; envelope protein; anti-HIV;
XX immune response; ss.

XX Synthetic.

XX WO200032802-A1.

XX 08-JUN-2000.

XX 25-NOV-1999; 99WO-GB03923.

XX 28-NOV-1998; 98GB-0026069.

XX (UYLE-) UNIV LEEDS;

XX Meredith DM, Markham AF;

XX WPI; 2000-412347/35.

XX Herpesvirus saimiri vector comprising a gene encoding an envelope
XX protein of human immunodeficiency virus (HIV), useful as a vaccine for
XX treating HIV infection and for delivering the protein to a specific
XX cell population -

XX Disclosure; Page 15; 33pp; English.

XX The present invention describes a herpesvirus saimiri (HVS) vector (I),
XX having part of a gene encoding an envelope protein of human
XX immunodeficiency virus (HIV), for delivering the protein to a specific
XX cell population. (I) is useful as a vaccine for inducing a humoral
XX and/or cellular anti-protein immune response to a T lymphocyte or
XX macrophage population, for manufacturing medicaments for preventing
XX and/or treating an individual likely to contract or suffering from HIV
XX infection, and for delivering selected HIV heterogeneous genetic
XX material to a specific cell population. The present sequence represents
XX an oligonucleotide which is used in the exemplification of the present
XX invention.

SQ Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 other;

Query Match 67.8%; Score 12.2; DB 21; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cggtacgtaagcctag 17

DB 1 cgcgacttaagcctag 17
||| |||||

RESULT 5
AAQ99545
ID AAQ99545 standard; DNA; 25 BP.

XX AC AAQ99545;

XX 28-FEB-1996 (first entry)

XX Human Fas ligand sense PCR primer-20.

XX Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
XX Fas cell surface antigen; human; Fas-L; ND38; truncated;
XX PCR primer; polymerase chain reaction; ss.

XX Synthetic.

XX WO9513293-A1.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-JP01899.

XX 18-OCT-1994; 94JP-0278378.

XX 10-NOV-1993; 93JP-0305975.

XX 13-DEC-1993; 93JP-0342526.

XX 18-MAR-1994; 94JP-0074344.

XX 08-JUL-1994; 94JP-0180955.

XX 07-SEP-1994; 94JP-0239363.

XX (MOCH) MOCHIDA PHARM CO LTD.

XX (OSAB-) OSAKA BIOSCIENCE INST.

XX Nagata S, Nakamura N, Suda T, Takahashi T;

XX WPI; 1995-194031/25.

XX Peptide which binds to Fas antigen, and antibody reactive with it -
XX for treatment and diagnosis of viral or auto-immune diseases
XX Example 22; Page 125; 300pp; Japanese.

XX The sense and antisense PCR primers in AAQ99545 and AAQ99546 were used
XX to amplify a human Fas ligand coding sequence for cloning in plasmid
XX pM1073. The plasmid was used for expressing the N-terminally
XX deleted Fas ligand ND38 in E.coli host cells.

XX Sequence 25 BP; 7 A; 8 C; 7 G; 3 T; 0 other;
Query Match 67.8%; Score 12.2; DB 16; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gttacgtaagcctagga 18
||||| |||||

DB 5 gttaccagaagccaagga 21
||||| |||||

RESULT 6
AAC73635
ID AAC73635 standard; DNA; 38 BP.

XX AC AAC73635;

XX 02-FEB-2001 (first entry)

XX Single base extension primer #141 used in multiplexing PCR/SBE assay.

XX Oligonucleotide array; genotyping; single base extension reaction; SBE;

KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
 XX Unidentified.
 OS
 PN W0200058516-A2.
 XX
 PD 05-OCT-2000.
 XX
 XX 27-MAR-2000; 2000W0-US08069.
 XX
 XX 26-MAR-1999; 99US-0126473.
 XX
 XX 23-JUN-1999; 99US-0140359.
 XX
 XX (WHTEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 XX
 XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
 PI Ryder T, Sklar P;
 XX WPI; 2000-656171/63.
 XX
 XX Universal array of oligonucleotides tags attached to a solid substrate
 PT along with locus-specific tagged oligonucleotides useful in genotyping
 PT using single base extension reactions -
 XX
 XX Example 7; Page 63; 83pp; English.
 PS
 XX The present invention relates to an oligonucleotide array comprising
 CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
 CC array is useful for genotyping a nucleic acid sample at one or more loci
 CC via single base extension (SBE) reactions. A pair of primers is used to
 CC amplify a polymorphic locus in a sample e.g. a single nucleotide
 CC polymorphism (SNP). The amplified nucleic acid product is then used as a
 CC template in a SBE reaction with an extension primer. The present sequence
 CC is one such SBE reaction primer used in the method of the present
 CC invention. The SBE reaction products are used to form the oligonucleotide
 CC array.
 XX
 XX Sequence 38 BP; 8 A; 10 C; 10 G; 10 T; 0 other;

Query Match 67.88; Score 12.2; DB 21; Length 38;
 Best Local Similarity 82.48; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagg 17
 |||||
 Db 7 cgttacgtagctctcgg 23

RESULT 7
 AAV56953/c
 ID AAV56953 standard; DNA; 18 BP.
 XX
 AC AAV56953;
 XX
 XX 02-DEC-1998 (first entry)
 XX
 XX Regulatory element containing oligonucleotide #112.
 XX
 KW Cytokine-responsive regulatory; primer; promoter; detection; isolation;
 KW transcriptional control; STAT protein; screening; agonist; ss.
 XX
 OS Synthetic.
 XX
 XX US5814517-A.
 XX
 XX 29-SEP-1998.
 XX
 XX 27-MAR-1995; 95US-0410779.
 XX
 XX 27-MAR-1995; 95US-0410779.
 XX
 XX 14-APR-1994; 94US-0228935.

XX (LIGA-) LIGAND PHARM INC.
 XX
 XX Lamb IP, Seidel HM;
 PI
 XX WPI; 1998-541763/46.
 XX
 XX DNA constructs containing cytokine-responsive regulatory elements -
 PT useful in assays for transcription-regulating proteins or gene
 PT transcription agonists or antagonists
 XX
 XX Example 2; Column 27-28; 58pp; English.
 PS
 XX
 XX AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
 CC production of constructs comprising a cytokine-responsive regulatory
 CC element linked to a promoter which is linked to a heterologous coding
 CC sequence so that the coding sequence is under the transcriptional
 CC control of the regulatory element and the promoter, where the regulatory
 CC element has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and
 CC TTCNVTAA where N is A, T, C or G, and Y = 3 or 4. The constructs can be
 CC used to detect or isolate transcription-regulating proteins, e.g. STAT
 CC proteins, in a sample by contacting the sample with the construct so that
 CC the protein binds to the regulatory element, and detecting or separating
 CC the resulting complex. The cells can be used in screening assays for
 CC agonists of gene transcription, in which the level of expression of the
 CC coding sequence is measured in the presence and absence of a test
 CC compound or in the presence of the corresponding cytokine.
 XX
 XX Sequence 18 BP; 4 A; 4 C; 4 G; 6 T; 0 other;
 SQ
 Query Match 66.7%; Score 12; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 cgttacgtaagc 12
 |||||
 Db 17 CGTTACGTAAGC 6
 RESULT 8
 AAV56954
 ID AAV56954 standard; DNA; 18 BP.
 XX
 AC AAV56954;
 XX
 XX 02-DEC-1998 (first entry)
 XX
 XX Regulatory element containing oligonucleotide #113.
 XX
 KW Cytokine-responsive regulatory; primer; promoter; detection; isolation;
 KW transcriptional control; STAT protein; screening; agonist; ss.
 XX
 OS Synthetic.
 XX
 XX US5814517-A.
 XX
 XX 29-SEP-1998.
 XX
 XX 27-MAR-1995; 95US-0410779.
 XX
 XX 27-MAR-1995; 95US-0410779.
 XX
 XX 14-APR-1994; 94US-0228935.
 XX
 XX (LIGA-) LIGAND PHARM INC.
 XX
 XX Lamb IP, Seidel HM;
 PI
 XX WPI; 1998-541763/46.
 XX
 XX DNA constructs containing cytokine-responsive regulatory elements -
 PT useful in assays for transcription-regulating proteins or gene
 PT transcription agonists or antagonists

XX Example 2; Column 27-28; 58pp; English.
 PS AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
 CC production of constructs comprising a cytokine-responsive regulatory
 CC element linked to a promoter which is linked to a heterologous coding
 CC sequence so that the coding sequence is under the transcriptional
 CC control of the regulatory element and the promoter, where the regulatory
 CC element has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and
 CC TTCNYTAA where N is A, T, C or G, and y = 3 or 4. The constructs can be
 CC used to detect or isolate transcription-regulating proteins, e.g. STAT
 CC proteins, in a sample by contacting the sample with the construct so that
 CC the protein binds to the regulatory element, and detecting or separating
 CC the resulting complex. The cells can be used in screening assays for
 CC agonists of gene transcription, in which the level of expression of the
 CC coding sequence is measured in the presence and absence of a test
 CC compound or in the presence of the corresponding cytokine.
 XX
 SQ Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 other;

Query Match 66.7%; Score 12; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggtacgtaagc 12
 |||||
 Db 6 cggtacgtaagc 17

RESULT 9
 AAQ14923
 ID AAQ14923 standard; DNA; 31 BP.
 XX
 AC AAQ14923;
 XX
 DT 17-MAR-1992 (first entry)
 XX
 DE CD46 exon 6-9 probe.
 XX
 KW Alternative splicing; splice variant; membrane cofactor protein;
 KW MCP; ss.
 XX
 OS Synthetic.
 XX
 PN WO9118097-A.
 XX
 XX 28-NOV-1991.
 PD
 PF 10-MAY-1991; 91WO-AU000199.
 XX
 PR 11-MAY-1990; 90AU-0000133.
 XX
 PA (UYME-) UNIV MELBOURNE.
 XX
 PI Purcell DEJ, Russell SM, McKenzie JFC;
 XX
 DR WPI; 1991-369251/50.
 XX
 PT New CD46 membrane cofactor protein variants - useful as probes
 PT to identify CD46 isoforms and for diagnosing spontaneous
 PT abortion, inhibiting immuno:response and treating leukaemia
 XX
 PS Disclosure; Page 22; 77pp; English.
 XX
 CC The probes represented in AAQ14921-25 and AAQ15211-12 were used to
 CC determine the tissue distribution of alternatively spliced CD46
 CC RNA transcripts.
 CC
 CC See also AAQ14915-25, AAQ15211-12 and AAR15457-59.
 XX
 SQ Sequence 31 BP; 9 A; 6 C; 7 G; 9 T; 0 other;

Query Match 65.6%; Score 11.8; DB 12; Length 31;
 Best Local Similarity 86.7%; Pred. No. 2.1e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 tacgtacgcttaga 18
 |||||
 Db 1 taagtacgcttaga 15
 RESULT 10
 AAL33677
 ID AAL33677 standard; DNA; 50 BP.
 XX
 AC AAL33677;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #6885.
 XX
 KW Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.

XX WO200147944-A2.
 PN
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;
 PI
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1; Page 3351; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

SQ Sequence 50 BP; 11 A; 9 C; 17 G; 13 T; 0 other;

Query Match 65.6%; Score 11.8; DB 22; Length 50;
 Best Local Similarity 86.7%; Pred. No. 2.2e+03;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tacgtaagccttaga 18
 ||||| |||||

Db 8 taagtggccttaga 22

RESULT 11
 ABI84598
 ID ABI84598 standard; DNA; 24 BP.
 XX ABI84598;
 AC
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide Zip ID#1101 oligo #1.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligation detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US10958.
 XX
 PR 14-APR-2000; 2000US-197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 25; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Brucella
 CC melitensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying (if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 24 BP; 5 A; 8 C; 5 G; 6 T; 0 other;

Query Match 64.4%; Score 11.6; DB 24; Length 24;

Best Local Similarity 77.8%; Pred. No. 2.7e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttaga 18
 ||||| |||||

Db 1 cgttacggaatccttga 18

RESULT 12
 ABI84599/C
 ID ABI84599 standard; DNA; 24 BP.
 XX ABI84599;
 AC
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide Zip ID#1101 oligo #2.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligation detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US10958.
 XX
 PR 14-APR-2000; 2000US-197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 25; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Brucella
 CC melitensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying (if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 24 BP; 6 A; 5 C; 8 G; 5 T; 0 other;

Query Match 64.4%; Score 11.6; DB 24; Length 24;
 Best Local Similarity 77.8%; Pred. No. 2.7e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
 Db 24 CGTTACGAATCCTTGA 7

RESULT 13
 AAC66117/c
 ID AAC66117 standard; DNA; 42 BP.
 XX
 AC AAC66117;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 DE PCR primer #3n+IR used in mutant protein library construction.
 KW Human; fibroblast growth factor; FGF; mutant protein library preparation;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN JP2000236880-A.
 XX
 PD 05-SEP-2000.
 XX
 PF 19-FEB-1999; 99JP-0041538.
 XX
 PR 19-FEB-1999; 99JP-0041538.
 XX
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 XX
 DR WPI; 2000-658507/64.
 XX
 PT Production of a mutant protein, preparation of a mutant protein library
 and preparation of a cDNA library encoding a mutant protein -
 XX
 PS Examples; Page 8; 36pp; Japanese.
 XX
 CC This invention relates to the preparation of a cDNA library encoding a
 mutant in which an amino acid or a peptide is introduced to a random site
 on the primary structure of a protein. The method comprises recombining
 cDNA encoding a protein to a cyclic plasmid and cleaving the cyclic
 plasmid at one random site and introducing a cDNA encoding an amino acid
 or a peptide at the cleaved site. The method is used to optimise protein
 mutation introduction rates. The present sequence represents a PCR primer
 used in an illustration of the method of the invention.
 XX
 SQ Sequence 42 BP; 9 A; 16 C; 7 G; 10 T; 0 other;

Query Match 64.4%; Score 11.6; DB 21; Length 42;
 Best Local Similarity 77.8%; Pred. No. 2.8e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
 Db 25 CGTAACTTAAGCCCGGA 8

RESULT 14
 AAX35090
 ID AAX35090 standard; cDNA; 50 BP.
 XX
 AC AAX35090;
 XX
 DT 01-JUL-1999 (first entry)
 XX
 DE Oligonucleotide which is internally functionalized.
 XX
 KW Internucleotide linkage; N-aminoalkyl phosphoramidate;

aminoalkyl group; internally labelled oligonucleotide analogue; ss.
 XX Synthetic.
 XX US5563253-A.
 XX
 PD 08-OCT-1996.
 XX
 PF 03-MAR-1994; 94US-0206175.
 XX
 PR 03-MAR-1994; 94US-0206175.
 PR 08-MAR-1990; 90US-0490481.
 XX
 PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.
 XX
 PI Agrawal S, Tang J;
 XX
 DR WPI; 1996-464214/46.
 XX
 PT Oligo:nucleotide analogues for internal labelling - containing
 aminoalkyl phosphoramidate inter:nucleotide linkages
 XX
 PS Example 1; Columns 7-8; 14pp; English.
 XX
 CC Oligonucleotides AAX35084-92 exemplify the invention. They represents
 oligonucleotide analogues which comprise a linear chain of 17-50
 nucleotides with at least one internucleotide linkage being an
 N-aminoalkyl phosphoramidate group. The aminoalkyl group can be
 labelled non-radioactively, e.g. with biotin, fluorescein or rhodamine,
 CC to provide internally labelled oligonucleotide analogues useful in
 research or in the diagnosis and treatment of diseases and conditions
 CC of interest.
 XX
 SQ Sequence 50 BP; 13 A; 11 C; 15 G; 11 T; 0 other;

Query Match 64.4%; Score 11.6; DB 17; Length 50;
 Best Local Similarity 77.8%; Pred. No. 2.9e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
 Db 1 cgatgcgtagcctagaa 18

RESULT 15
 AAT41692
 ID AAT41692 standard; DNA; 50 BP.
 XX
 AC AAT41692;
 XX
 DT 05-DEC-1996 (first entry)
 XX
 DE Oligonucleotide containing aminoalkylphosphotriester linkage.
 XX
 KW aminoalkylphosphotriester; internally functionalised; linkage;
 KW diagnosis; non-radioactively labelled; ss.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT misc_difference 1..50
 FT /*tag= a
 FT /note= "at least one linkage along the chain is an
 aminoalkylphosphotriester residue of
 structure -Nu2-O-P(O)[O(CH2)nNH2]-O-Nu1-
 (where n is 2-6 and Nu1 and Nu2 are the
 adjacent nucleosides) to which a
 non-radioactive label can be attached"

US5541305-A.
 30-JUL-1996.

XX 16-DEC-1994; 94US-0357666.
XX 03-MAR-1994; 94US-0206175.
PR 08-MAR-1990; 90US-0490481.
PR 16-DEC-1994; 94US-0357666.
XX (WORC-) WORCESTER FOUND BIOMEDICAL RES.
XX Agrawal S, Tang J;
XX WPI; 1996-362016/36.
XX New oligo:nucleotide derivs. - having aminoalkyl:phospho:tri:ester
PT inter:nucleoside linkage which can be labelled or functionalised
XX Examples; Column 8; 14pp; English.
XX The invention relates to a compound consisting of 5-50 covalently linked
CC nucleosides in which at least one linkage between the nucleosides is
CC through an aminoalkyl phosphotriester residue having the formula
CC -Nu2-O-P(O)[O(CH2)nNH2]-O-Nu1-, where n is 2-6 and Nu1 and Nu2 are
CC those nucleosides adjacent to the residue. The amino group of the
CC modified linkage can be used to attach a non-radioactive label such as
CC biotin, fluorescein or rhodamine or their derivatives, so that the label
CC is attached at a predetermined position. The non-radioactively labelled
CC compound is useful in research and in the diagnosis and treatment of
CC diseases and conditions of interest. The present sequence is a specific
CC example of an oligonucleotide which incorporates the modified linkage.
XX
SQ Sequence 50 BP; 13 A; 11 C; 15 G; 11 T; 0 other;

Query Match 64.4%; Score 11.6; DB 17; Length 50;
Best Local Similarity 77.8%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 cgttacgtaagcctagga 18
||| |||||
Db 1 cgatgcgtaggcctagaa 18

Search completed: October 12, 2002, 17:08:03
Job time: 9748 sec

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:36 ; Search time 191.26 Seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-4

Perfect score: 18

Sequence: 1 cgttacgtaagcctagga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
c 1	12.8	71.1	20	4	US-09-593-711A-133
c 2	12.2	67.8	25	4	US-08-339-214-101
c 3	12	66.7	18	1	US-08-410-779B-112
c 4	12	66.7	18	1	US-08-410-779B-113
c 5	12	66.7	18	5	PCT-US95-04477-112
c 6	12	66.7	18	5	PCT-US95-04477-113
c 7	11.8	65.6	19	1	US-08-623-195-19
c 8	11.8	65.6	31	2	US-08-528-057-35
c 9	11.8	65.6	42	2	US-08-528-057-19
c 10	11.6	64.4	50	1	US-08-357-399-10
c 11	11.6	64.4	50	1	US-08-357-666-10
c 12	11.6	64.4	50	1	US-08-206-175-10
c 13	11.4	63.3	22	4	US-09-043-507-4
c 14	11.4	63.3	31	3	US-08-542-051-39
c 15	11.4	63.3	35	3	US-08-542-051-37
c 16	11.4	63.3	45	3	US-08-860-368B-8
c 17	11.4	63.3	47	1	US-08-435-480-7
c 18	11.2	62.2	20	4	US-09-593-711A-36
c 19	11.2	62.2	25	1	US-08-182-961B-15
c 20	11.2	62.2	25	4	US-09-007-678B-15
c 21	11.2	62.2	27	2	US-08-244-434-13
c 22	11.2	62.2	29	1	US-07-631-717A-2
c 23	11.2	62.2	29	1	US-08-306-255-5
c 24	11.2	62.2	29	1	US-08-166-717B-2
c 25	11.2	62.2	32	4	US-09-215-098-1
c 26	11.2	62.2	34	2	US-08-343-923-2
c 27	11.2	62.2	35	2	US-08-244-434-12

c 28	11.2	62.2	35	2	US-08-244-434-16	Sequence 16, Appl
c 29	11.2	62.2	37	4	US-09-025-769B-112	Sequence 112, App
c 30	11.2	62.2	40	2	US-09-130-114-18	Sequence 18, Appl
c 31	11.2	62.2	44	2	US-09-130-114-17	Sequence 17, Appl
c 32	11	61.1	21	2	US-08-855-449-8	Sequence 8, Appl
c 33	11	61.1	30	2	US-08-396-927A-3	Sequence 3, Appl
c 34	10.8	60.0	16	4	US-09-156-828B-24	Sequence 24, Appl
c 35	10.8	60.0	20	1	US-07-906-930B-20	Sequence 20, Appl
c 36	10.8	60.0	20	3	US-08-574-396-40	Sequence 40, Appl
c 37	10.8	60.0	20	3	US-08-310-259B-14	Sequence 14, Appl
c 38	10.8	60.0	20	4	US-08-973-568-40	Sequence 40, Appl
c 39	10.8	60.0	21	1	US-08-093-741-29	Sequence 29, Appl
c 40	10.8	60.0	21	1	US-08-720-012-29	Sequence 29, Appl
c 41	10.8	60.0	21	4	US-09-156-828B-22	Sequence 22, Appl
c 42	10.8	60.0	22	3	US-08-477-934-27	Sequence 27, Appl
c 43	10.8	60.0	29	1	US-08-093-741-30	Sequence 30, Appl
c 44	10.8	60.0	29	1	US-08-720-012-30	Sequence 30, Appl
c 45	10.8	60.0	30	2	US-08-528-057-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-593-711A-133/c
; Sequence 133, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RYS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-711A-133

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 68;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gttacgtaagcctagg 17
Db 17 GTTACGTAGCCTCGG 2
||||| ||||| ||

RESULT 2
US-08-339-214-101
; Sequence 101, Application US/08339214
; Patent No. 6348334
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigikazu
; APPLICANT: Suda, Takashi
; APPLICANT: Takahashi, Tomoniro
; APPLICANT: Nakamura, No. 634833410
; TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
; TITLE OF INVENTION: Encoding the Same
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,214
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-139P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sense primer 20"
; ANTI-SENSE: NO
; US-08-339-214-101

Query Match 67.8%; Score 12.2; DB 4; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttacgtgaagccctagga 18
||||| ||||| |||||
Db 5 GTTACCAAGCCCAAGGA 21

RESULT 3
US-08-410-779B-112/c
; Sequence 112, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906

; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; US-08-410-779B-112

Query Match 66.7%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cgttacgtaagc 12
||||| ||||| |||||
Db 17 CGTTACGTAAGC 6

RESULT 4
US-08-410-779B-113
; Sequence 113, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; US-08-410-779B-113

Query Match 66.7%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttacgtaagc 12
|||||
Db 6 CGTTACGTAAGC 17

RESULT 5
PCT-US95-04477-112/c
; Sequence 112, Application PC/TUS9504477
; GENERAL INFORMATION:
; APPLICANT: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
; TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 165
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; SYNTHETIC DNA"
PCT-US95-04477-112

Query Match 66.7%; Score 12; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttacgtaagc 12
|||||
Db 17 CGTTACGTAAGC 6

RESULT 6
PCT-US95-04477-113
; Sequence 113, Application PC/TUS9504477
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
; NUMBER OF SEQUENCES: 165
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; SYNTHETIC DNA"
PCT-US95-04477-113

Query Match 66.7%; Score 12; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttacgtaagc 12
|||||
Db 6 CGTTACGTAAGC 17

RESULT 7
US-08-623-195-19/G
; Sequence 19, Application US/08623195
; Patent No. 5759810
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITO, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,195
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 71033/1995
; FILING DATE: 29-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 029430-293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-623-195-19

Query Match 65.6%; Score 11.8; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 tacgtaagcctagga 18
|||||
Db 15 TACTTAAGCCAAGGA 1

RESULT 8
US-08-528-057-35
; Sequence 35, Application US/08528057

; Patent No. 5846715
; GENERAL INFORMATION:
; APPLICANT: PURCELL, Damian F. J.
; APPLICANT: RUSSELL, Sarah M.
; APPLICANT: MCKENZIE, Ian F. C.
; TITLE OF INVENTION: CD46 VARIANTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/528.057
; FILING DATE: CONCURRENTLY HEREWITH
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/961.686
; FILING DATE: 11-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU91/00199
; FILING DATE: 10-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK0133/90
; FILING DATE: 11-MAY-1990
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/112 DACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: exons 6-9
US-08-528-057-35

Query Match 65.6%; Score 11.8; DB 2; Length 31;
Best Local Similarity 86.7%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tacgtagccttagga 18
||| ||| ||| ||| |||
Db 1 TAAAGTAGCCTTAGGA 15

RESULT 9
US-08-528-057-19/c
; Sequence 19, Application US/08528057
; Patent No. 5846715
; GENERAL INFORMATION:
; APPLICANT: PURCELL, Damian F. J.
; APPLICANT: RUSSELL, Sarah M.
; APPLICANT: MCKENZIE, Ian F. C.
; TITLE OF INVENTION: CD46 VARIANTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/528.057
; FILING DATE: CONCURRENTLY HEREWITH
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/961.686
; FILING DATE: 11-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU91/00199
; FILING DATE: 10-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK0133/90
; FILING DATE: 11-MAY-1990
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/112 DACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: exon 9
US-08-528-057-19

Query Match 65.6%; Score 11.8; DB 2; Length 42;
Best Local Similarity 86.7%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tacgtagccttagga 18
||| ||| ||| ||| |||
Db 16 TAAAGTAGCCTTAGGA 2

RESULT 10
US-08-357-399-10
; Sequence 10, Application US/08357399
; Patent No. 5536821
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; APPLICANT: Tang, Jin-Yan
; TITLE OF INVENTION: Site-Specific Functionalization of
; TITLE OF INVENTION: Oligodeoxynucleotides for
; TITLE OF INVENTION: No. 5536821-Radioactive Labelling
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357.399

```
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206175
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-014CPDV2
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-357-399-10
```

```
Query Match 64.4%; Score 11.6; DB 1; Length 50;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 cgttacgtaagcctagga 18
||| ||||| ||||| |
Db 1 CGATGCGTAGGCGCTAGAA 18
```

```
RESULT 11
US-08-357-666-10
; Sequence 10, Application US/08357666
; Patent No. 5541306
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; APPLICANT: Tang, Jin-Yan
; TITLE OF INVENTION: Site-Specific Functionalization of
; TITLE OF INVENTION: Oligodeoxynucleotides for
; TITLE OF INVENTION: No. 5541306-Radioactive Labelling
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,666
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206175
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-014CPDV1
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-357-666-10
```

```
Query Match 64.4%; Score 11.6; DB 1; Length 50;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 cgttacgtaagcctagga 18
||| ||||| ||||| |
Db 1 CGATGCGTAGGCGCTAGAA 18
```

```
RESULT 12
US-08-206-175-10
; Sequence 10, Application US/08206175
; Patent No. 5563253
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir and
; APPLICANT: Jin-Yan Tang
; TITLE OF INVENTION: Site-Specific Functionalization of
; TITLE OF INVENTION: Oligodeoxynucleotides for
; TITLE OF INVENTION: No. 5563253-Radioactive Labelling
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,175
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-014 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-206-175-10
```

```
Query Match 64.4%; Score 11.6; DB 1; Length 50;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 cgttacgtaagcctagga 18
||| ||||| ||||| |
Db 1 CGATGCGTAGGCGCTAGAA 18
```

RESULT 13
US-09-043-507-4/c
; Sequence 4, Application US/09043507
; Patent No. 6165716
; GENERAL INFORMATION:
; APPLICANT: BATTERSBY, SHARON
; APPLICANT: FINK, GEORGE
; APPLICANT: GOODWIN, GUY MANNING
; APPLICANT: HARMAR, ANTHONY JOHN
; APPLICANT: OGILVIE, ALAN DAVID
; APPLICANT: SMITH, CHRISTOPHER
; TITLE OF INVENTION: SCREENING FOR DISORDERS OF
; TITLE OF INVENTION: SEROTONERGIC DYSFUNCTION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,507
; FILING DATE: 23-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/02360
; FILING DATE: 23-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: RATNER, ALLAN
; REGISTRATION NUMBER: 19,717
; REFERENCE/DOCKET NUMBER: MUR-7060
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-043-507-4

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 cgttaagcctagga 18
||| ||| ||| |||
Db 16 CGTAAGACTAGGA 4

RESULT 14
US-08-542-051-39
; Sequence 39, Application US/08542051F
; Patent No. 6004782
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; APPLICANT: McPherson, David T.
; APPLICANT: Urry, Dan W.
; APPLICANT: Xu, Jie
; TITLE OF INVENTION: Hyperexpression of Bioelastic Polypeptides
; FILE REFERENCE: BERL-018/01US
; CURRENT APPLICATION NUMBER: US/08/542,051F
; CURRENT FILING DATE: 1995-10-13

; EARLIER APPLICATION NUMBER: 08/423,642
; EARLIER FILING DATE: 1995-04-14
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-08-542-051-39

Query Match 63.3%; Score 11.4; DB 3; Length 31;
Best Local Similarity 92.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 acgtaagcctagg 17
||| ||| ||| |||
Db 17 acttaagcctagg 29

RESULT 15
US-08-542-051-37
; Sequence 37, Application US/08542051F
; Patent No. 6004782
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; APPLICANT: McPherson, David T.
; APPLICANT: Urry, Dan W.
; APPLICANT: Xu, Jie
; TITLE OF INVENTION: Hyperexpression of Bioelastic Polypeptides
; FILE REFERENCE: BERL-018/01US
; CURRENT APPLICATION NUMBER: US/08/542,051F
; CURRENT FILING DATE: 1995-10-13
; EARLIER APPLICATION NUMBER: 08/423,642
; EARLIER FILING DATE: 1995-04-14
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-08-542-051-37

Query Match 63.3%; Score 11.4; DB 3; Length 35;
Best Local Similarity 92.3%; Pred. No. 4.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 acgtaagcctagg 17
||| ||| ||| |||
Db 21 acttaagcctagg 33

Search completed: October 12, 2002, 16:54:36
Job time: 8991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:30 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-4
Perfect score: 18
Sequence: 1 cgttacgtaagcctagga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 1081749327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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- 2: /cgn2_6/ptodata/2/pna/US06_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_COMB.seq.*
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- 12: /cgn2_6/ptodata/2/pna/US088_COMB.seq.*
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- 21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq.*
- 22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq.*
- 23: /cgn2_6/ptodata/2/pna/US096A_COMB.seq.*
- 24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq.*
- 25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq.*
- 26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq.*
- 27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq.*
- 28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq.*
- 29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq.*
- 30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq.*
- 31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq.*
- 32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq.*
- 33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq.*
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- 39: /cgn2_6/ptodata/2/pna/US6000_COMB.seq.*
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- 41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq.*
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- 45: /cgn2_6/ptodata/2/pna/US6006_COMB.seq.*
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- 47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq.*
- 48: /cgn2_6/ptodata/2/pna/US6009_COMB.seq.*
- 49: /cgn2_6/ptodata/2/pna/US6010_COMB.seq.*
- 50: /cgn2_6/ptodata/2/pna/US6011_COMB.seq.*
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- 53: /cgn2_6/ptodata/2/pna/US6014_COMB.seq.*
- 54: /cgn2_6/ptodata/2/pna/US6015_COMB.seq.*
- 55: /cgn2_6/ptodata/2/pna/US6016_COMB.seq.*
- 56: /cgn2_6/ptodata/2/pna/US6017_COMB.seq.*
- 57: /cgn2_6/ptodata/2/pna/US6018_COMB.seq.*
- 58: /cgn2_6/ptodata/2/pna/US6019_COMB.seq.*
- 59: /cgn2_6/ptodata/2/pna/US6020_COMB.seq.*
- 60: /cgn2_6/ptodata/2/pna/US6021_COMB.seq.*
- 61: /cgn2_6/ptodata/2/pna/US6022_COMB.seq.*
- 62: /cgn2_6/ptodata/2/pna/US6023_COMB.seq.*
- 63: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
- 64: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
- 65: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
- 66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
- 67: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*
- 68: /cgn2_6/ptodata/2/pna/US6029_COMB.seq.*
- 69: /cgn2_6/ptodata/2/pna/US6030_COMB.seq.*
- 70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
- 71: /cgn2_6/ptodata/2/pna/US6032_COMB.seq.*
- 72: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
- 73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	18	16	US-09-241-561-4	Sequence 4, Appli
c	14.4	80.0	25	74	US-60-353-987-681647	Sequence 681647,
3	13.8	76.7	25	62	US-60-232-638-76423	Sequence 76423, A
4	13.8	76.7	25	74	US-60-353-987-755566	Sequence 755566,
5	13.8	76.7	25	74	US-60-353-987-755567	Sequence 755567,
6	13.8	76.7	25	74	US-60-353-987-755568	Sequence 755568,
c	13.4	74.4	25	35	US-09-954-427-408320	Sequence 408320,
c	13.4	74.4	25	62	US-60-233-166-408320	Sequence 408320,
c	13.2	73.3	25	35	US-09-956-584-493346	Sequence 493346,
10	13.2	73.3	25	62	US-60-233-620-86428	Sequence 86428, A
11	13.2	73.3	25	62	US-60-233-620-86434	Sequence 86434, A
12	13.2	73.3	25	62	US-60-234-017-481562	Sequence 481562,
13	13.2	73.3	25	74	US-60-353-987-21692	Sequence 21692, A
c	13.2	73.3	25	74	US-60-353-987-104566	Sequence 104566,
c	13.2	73.3	25	74	US-60-353-987-586958	Sequence 586958,
16	13.2	73.3	25	74	US-60-353-987-831824	Sequence 831824,
17	13.2	73.3	26	1	PCT-US94-12505-10	Sequence 10, Appl
18	13.2	73.3	26	5	US-08-142-124-10	Sequence 10, Appl
19	13.2	73.3	26	15	US-09-114-911-10	Sequence 10, Appl
20	13	72.2	25	74	US-60-353-987-506710	Sequence 506710,
c	13	72.2	32	16	US-09-238-351-7	Sequence 7, Appli
c	13	72.2	32	16	US-09-238-351-3	Sequence 3, Appli
c	13	72.2	33	16	US-09-621-275-3	Sequence 3, Appli
c	12.8	71.1	20	1	PCT-US01-18763A-133	Sequence 133, App
c	12.8	71.1	25	62	US-60-234-049-20336	Sequence 20336, A
c	12.8	71.1	25	74	US-60-353-987-163602	Sequence 163602,
c	12.8	71.1	25	74	US-60-353-987-219543	Sequence 219543,
c	12.8	71.1	25	74	US-60-353-987-219780	Sequence 219780,
c	12.8	71.1	25	74	US-60-353-987-533823	Sequence 533823,
c	12.8	71.1	25	74	US-60-353-987-533824	Sequence 533824,

c 32 12.8 71.1 25 74 US-60-353-987-533825 Sequence 533825,
c 33 12.8 71.1 25 74 US-60-353-987-681648 Sequence 681648,
c 34 12.8 71.1 25 74 US-60-353-987-733622 Sequence 733622,
c 35 12.8 71.1 25 74 US-60-353-987-782764 Sequence 782764,
c 36 12.8 71.1 34 16 US-09-254-326-4 Sequence 4, Appl1
c 37 12.8 71.1 34 32 US-09-856-652-6 Sequence 6, Appl1
c 38 12.8 71.1 47 60 US-60-216-745-2749 Sequence 2749, Ap
c 39 12.4 68.9 25 26 US-09-660-220-73594 Sequence 73594, A
c 40 12.4 68.9 25 35 US-09-954-427-56195 Sequence 56195, A
c 41 12.4 68.9 25 35 US-09-954-427-56196 Sequence 56196, A
c 42 12.4 68.9 25 35 US-09-954-427-288140 Sequence 288140,
c 43 12.4 68.9 25 35 US-09-956-584-262356 Sequence 262356,
c 44 12.4 68.9 25 35 US-09-956-584-363799 Sequence 363799,
c 45 12.4 68.9 25 62 US-60-232-638-30976 Sequence 30976, A

ALIGNMENTS

RESULT 1
US-09-241-561-4
; Sequence 4, Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-4

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 18
|||||
Db 1 cgttacgtaagcctagg 18

RESULT 2
US-60-353-987-681647/c
; Sequence 681647, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: MITTMANN, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 681647
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-681647

Query Match 80.0%; Score 14.4; DB 74; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ttacgtaagcctagg 18
|||||
Db 24 TTACGTAAGCCTAGAA 9

RESULT 3
US-60-232-638-76423
; Sequence 76423, Application US/60232638
; GENERAL INFORMATION:
; APPLICANT: MITTMANN
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76423
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cervisiae
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YHR106W
US-60-232-638-76423

Query Match 76.7%; Score 13.8; DB 62; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 17
|||||
Db 8 cgttacgtaggcctgg 24

RESULT 4
US-60-353-987-755566
; Sequence 755566, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: MITTMANN, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 755566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-755566

Query Match 76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 17
|||||
Db 3 cgttacgtaagcctagg 19

RESULT 5
US-60-353-987-755567
; Sequence 755567, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: MITTMANN, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33

; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353.987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 755567
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-60-353-987-755567

Query Match 76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 17
|||||
Db 3 cgttacgtaagcagagg 19

RESULT 6
US-60-353-987-755568
; Sequence 755568, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353.987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 755568
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-60-353-987-755568

Query Match 76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 17
|||||
Db 3 cgttacgtaagcagagg 19

RESULT 7
US-09-954-427-408320/c
; Sequence 408320, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954.427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 408320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccaromyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-09-954-427-408320

Query Match 74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 tacgtaagcctagg 18
|||||
Db 23 TACGTAAGCCTAAGA 9

RESULT 8
US-60-233-166-408320/c
; Sequence 408320, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233.166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 408320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccaromyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-60-233-166-408320

Query Match 74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 tacgtaagcctagg 18
|||||
Db 23 TACGTAAGCCTAAGA 9

RESULT 9
US-09-956-584-493346/c
; Sequence 493346, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956.584
; CURRENT FILING DATE: 2001-09-19
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 493346
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-493346

Query Match 73.3%; Score 13.2; DB 35; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 18
|||||
Db 19 CGTTACTTAATCCTAAGA 2

RESULT 10
US-60-233-620-86428
; Sequence 86428, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of

; TITLE OF INVENTION: Arabidopsis thaliana
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC006136
US-60-233-620-86428

Query Match 73.3%; Score 13.2; DB 62; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 2 cgttatgtagaccttaga 19
||||| ||| |||||

RESULT 11

US-60-233-620-86434
; Sequence 86434, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; Arabidopsis thaliana
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86434
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC006136
US-60-233-620-86434

Query Match 73.3%; Score 13.2; DB 62; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 5 cgttatgtagaccttaga 22
||||| ||| |||||

RESULT 12

US-60-234-017-481562/c
; Sequence 481562, Application US/602334017
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AI662159
US-60-234-017-481562

Query Match 73.3%; Score 13.2; DB 62; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 19 CGTTACTTAATCCTAAGA 2
||||| ||| |||||

RESULT 13

US-60-353-987-21692/c
; Sequence 21692, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-21692

Query Match 73.3%; Score 13.2; DB 74; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 22 CGTATCGTAAGCCTTGA 5
||||| ||| |||||

RESULT 14

US-60-353-987-104566
; Sequence 104566, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 104566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-104566

Query Match 73.3%; Score 13.2; DB 74; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 3 cgttacctaagcccgga 20
||||| ||| |||||

RESULT 15

US-60-353-987-586958/c
; Sequence 586958, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133

; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 586958
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-586958

Query Match 73.3%; Score 13.2; DB 74; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 cgttacgtaagccttagga 18
 ||||| ||||| |||||
Db 21 CGTTTCGTAACCCCTGGGA 4

Search completed: October 12, 2002, 20:42:31
Job time: 16401 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:29 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-4

Perfect score: 18

Sequence: 1 cgttacgtaagcctagga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
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3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-4
2	13.2	73.3	25	6	US-10-215-112-1181
3	13.2	73.3	25	6	US-10-215-112-8531
4	13.2	73.3	26	5	US-09-668-890-10
5	12.8	71.1	25	5	US-09-956-604-2873
6	12.8	71.1	25	6	US-10-215-112-10029
7	12.2	67.8	25	5	US-09-956-604-96488
8	12.2	67.8	25	5	US-09-956-604-96547
9	12.2	67.8	25	6	US-10-215-112-642
10	12.2	67.8	25	6	US-10-215-112-3773
11	12	66.7	22	5	US-09-777-798-1
12	12	66.7	25	6	US-10-215-112-3998
13	12	66.7	25	6	US-10-215-112-11520
14	12	66.7	25	6	US-10-215-112-12848
15	11.8	65.6	24	1	PCT-US02-09558-2
16	11.8	65.6	25	5	US-09-956-604-96487
17	11.8	65.6	25	5	US-09-956-604-128739
18	11.8	65.6	25	5	US-09-396-196G-95431
19	11.8	65.6	25	5	US-09-396-196G-95432
20	11.6	64.4	25	5	US-09-956-604-108431
21	11.6	64.4	25	5	US-09-956-604-123143
22	11.6	64.4	25	5	US-09-396-196G-13193
23	11.6	64.4	25	5	US-09-396-196G-29737
24	11.6	64.4	25	5	US-09-396-196G-29748
25	11.6	64.4	25	6	US-10-215-112-1290

Sequence 8657, Ap
Sequence 28723, A
Sequence 28724, A
Sequence 28725, A
Sequence 28726, A
Sequence 28727, A
Sequence 28728, A
Sequence 28774, A
Sequence 28775, A
Sequence 28776, A
Sequence 28777, A
Sequence 28778, A
Sequence 28779, A
Sequence 28780, A
Sequence 28787, A
Sequence 55248, A
Sequence 55249, A
Sequence 33, Appli
Sequence 5, Appli
Sequence 13, Appli

US-10-215-112-8657
US-09-956-604-28723
US-09-956-604-28724
US-09-956-604-28725
US-09-956-604-28726
US-09-956-604-28727
US-09-956-604-28728
US-09-956-604-28774
US-09-956-604-28775
US-09-956-604-28776
US-09-956-604-28777
US-09-956-604-28778
US-09-956-604-28779
US-09-956-604-28780
US-09-956-604-28787
US-09-396-196G-55248
US-09-396-196G-55249
PCT-US02-16308-33
US-10-018-997-5
US-10-018-997-13

26 11.6 64.4 25 6
27 11.4 63.3 25 5
28 11.4 63.3 25 5
29 11.4 63.3 25 5
30 11.4 63.3 25 5
31 11.4 63.3 25 5
32 11.4 63.3 25 5
33 11.4 63.3 25 5
34 11.4 63.3 25 5
35 11.4 63.3 25 5
36 11.4 63.3 25 5
37 11.4 63.3 25 5
38 11.4 63.3 25 5
39 11.4 63.3 25 5
40 11.4 63.3 25 5
41 11.4 63.3 25 5
42 11.4 63.3 25 5
43 11.4 63.3 30 1
44 11.4 63.3 34 7
45 11.4 63.3 34 7

ALIGNMENTS

RESULT 1
US-09-945-131-4
; Sequence 4, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-4

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0

Oy 1 cgttacgtaagcctagga 18
| | | | | | | | | | | | | | | | | |
Db 1 cgttacgtaagcctagga 18

RESULT 2
US-10-215-112-1181
; Sequence 1181, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112

; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1181
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-1181

Query Match 73.3%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttagga 18
||| | ||||| |||||
Db 6 cgtgatgtaagcgttagga 23

RESULT 3
US-10-215-112-8531/c
; Sequence 8531, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-8531

Query Match 73.3%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttagga 18
||| | ||||| |||||
Db 20 CGTGATGTAGCGGTAGGA 3

RESULT 4
US-09-666-890-10
; Sequence 10, Application US/09666890
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Nucleic Acid Marker Ladder For
; Estimating Mass
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/666,890

; FILING DATE: 14-Jul-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,124
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.2570000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-666-890-10

Query Match 73.3%; Score 13.2; DB 5; Length 26;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttagga 18
||| | ||||| |||||
Db 6 CGTGAGGTGAGCCGTAGGA 23

RESULT 5
US-09-956-604-2873/c
; Sequence 2873, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 2873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-2873

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttag 16
||| | ||||| |||||
Db 23 CGITGCGGAAGCCTAG 8

RESULT 6
US-10-215-112-10029/c
; Sequence 10029, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10029

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10029

Query Match 71.1%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctag 16
||||| ||||| |||||
Db 25 CGTTTCGTAAGACTAG 10

RESULT 7
US-09-956-604-96488
; Sequence 96488, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 96488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-96488

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gttacgtaagcctagga 18
||||| ||||| |||||
Db 9 gttacgtaagcctagta 25

RESULT 8
US-09-956-604-96547/c
; Sequence 96547, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 96547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-96547

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gttacgtaagcctagga 18
||||| ||||| |||||
Db 24 GTTAAGTAAGTCTAGTA 8

RESULT 9
US-10-215-112-642
; Sequence 642, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-642

Query Match 67.8%; Score 12.2; DB 6; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctag 17
||||| ||||| |||||
Db 9 cgtgatgtaagcctag 25

RESULT 10
US-10-215-112-3773/c
; Sequence 3773, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3773
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-3773

Query Match 67.8%; Score 12.2; DB 6; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctag 17
||||| ||||| |||||
Db 17 CGTGATGTAAGCGTAGG 1

RESULT 11
US-09-777-798-1
; Sequence 1, Application US/09777798
; GENERAL INFORMATION:
; APPLICANT: Thompson, Steven A.
; APPLICANT: Cui, Cory
; APPLICANT: Clayton, Kathryn
; APPLICANT: Ernst, Cynthia
; TITLE OF INVENTION: HIGH OIL MAIZE PLANTS, AND METHODS FOR OBTAINING SAME
; FILE REFERENCE: DowAg/7094-143
; CURRENT APPLICATION NUMBER: US/09/777,798

; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-777-798-1

Query Match 66.7%; Score 12; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 acgtaagcctagg 16
|||||
Db 2 acgtaagcctagg 13

RESULT 12
US-10-215-112-3998
; Sequence 3998, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3998
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-3998

Query Match 66.7%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagg 17
|||||
Db 9 cgtaagcctagg 20

RESULT 13
US-10-215-112-11520
; Sequence 11520, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-11520

Query Match 66.7%; Score 12; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagg 17
|||||
Db 11 cgtaagcctagg 22

RESULT 14
US-10-215-112-12848
; Sequence 12848, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12848

Query Match 66.7%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagg 17
|||||
Db 5 cgtaagcctagg 16

RESULT 15
PCT-US02-09558-2/c
; Sequence 2, Application PC/TUS0209558
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; TITLE OF INVENTION: Ras p27 Animal Models and Uses Thereof
; FILE REFERENCE: USF-111XC1
; CURRENT APPLICATION NUMBER: PCT/US02/09558
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/278,430
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
PCT-US02-09558-2

Query Match 65.6%; Score 11.8; DB 1; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ttacgtaagcctagg 17
|||||
Db 16 TTAAGCCTGG 2

Search completed: October 12, 2002, 17:27:30
Job time: 10805 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:51:17 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: US-09-945-131-6

Perfect score: 18
Sequence: 1 catgtctccacacttga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_em.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	6	I33924	18	6	I33924	I33924 Sequence 2
2	13.8	76.7	33	6	A76106	33	6	A76106	A76106 Sequence 45
c 3	13.8	76.7	41	6	I68632	41	6	I68632	I68632 Sequence 5
c 4	13.2	73.3	33	6	AR014169	33	6	AR014169	AR014169 Sequence
c 5	13.2	73.3	36	6	AX069513	36	6	AX069513	AX069513 Sequence
c 6	13.2	73.3	36	6	AX069514	36	6	AX069514	AX069514 Sequence
c 7	12.8	71.1	20	12	AB068808	20	12	AB068808	AB068808 Synthetic
c 8	12.8	71.1	23	6	AX002948	23	6	AX002948	AX002948 Sequence
c 9	12.8	71.1	24	9	AX002963	24	9	AX002963	AX002963 Sequence
c 10	12.8	71.1	24	9	HSAT270350	24	9	HSAT270350	AJ770350 Homo sapi
c 11	12.8	71.1	28	6	AR090768	28	6	AR090768	AR090768 Sequence
c 12	12.8	71.1	28	6	AX350231	28	6	AX350231	AX350231 Sequence
c 13	12.8	71.1	33	6	A84409	33	6	A84409	AB4409 Sequence 24
c 14	12.8	71.1	35	23	E11199	35	23	E11199	E11199 Probe. 9/20
c 15	12.8	71.1	48	6	AX223672	48	6	AX223672	AX223672 Sequence
c 16	12.8	71.1	48	6	AX274473	48	6	AX274473	AX274473 Sequence
c 17	12.4	68.9	18	6	AR128932	18	6	AR128932	AR128932 Sequence
c 18	12.4	68.9	23	6	AR105887	23	6	AR105887	AR105887 Sequence
c 19	12.4	68.9	27	6	AR138967	27	6	AR138967	AR138967 Sequence
c 20	12.4	68.9	45	6	AR083218	45	6	AR083218	AR083218 Sequence
c 21	12.4	68.9	45	6	AR083219	45	6	AR083219	AR083219 Sequence
c 22	12.4	68.9	50	6	I42221	50	6	I42221	I42221 Sequence 34
c 23	12.2	67.8	21	6	E07342	21	6	E07342	E07342 Primer for
c 24	12.2	67.8	23	6	AX327683	23	6	AX327683	AX327683 Sequence
c 25	12.2	67.8	24	6	AX019226	24	6	AX019226	AX019226 Sequence
c 26	12.2	67.8	25	6	AR165197	25	6	AR165197	AR165197 Sequence
c 27	12.2	67.8	45	6	A47620	45	6	A47620	A47620 Sequence 12
c 28	12.2	67.8	45	6	A80120	45	6	A80120	A80120 Sequence 12
c 29	12.2	67.8	45	6	AX306498	45	6	AX306498	AX306498 Sequence
c 30	12.2	67.8	45	6	I34331	45	6	I34331	I34331 Sequence 30
c 31	12.2	67.8	47	6	AR088055	47	6	AR088055	AR088055 Sequence
c 32	12.2	67.8	47	6	AR088056	47	6	AR088056	AR088056 Sequence
c 33	12.2	67.8	50	6	AX164819	50	6	AX164819	AX164819 Sequence
c 34	12.2	67.8	50	9	HSATJ4655	50	9	HSATJ4655	AJ224655 Homo sapi
c 35	12	66.7	25	1	S58559	25	1	S58559	S58559 tRNA(GCAla
c 36	12	66.7	30	6	A62004	30	6	A62004	A62004 Sequence 34
c 37	12	66.7	30	6	AR125838	30	6	AR125838	AR125838 Sequence
c 38	12	66.7	30	6	I47250	30	6	I47250	I47250 Sequence 18
c 39	12	66.7	31	6	AR112518	31	6	AR112518	AR112518 Sequence
c 40	12	66.7	31	6	BD002606	31	6	BD002606	BD002606 Gene comp
c 41	11.8	65.6	19	12	AB069342	19	12	AB069342	AB069342 Synthetic
c 42	11.8	65.6	19	12	AB069344	19	12	AB069344	AB069344 Synthetic
c 43	11.8	65.6	20	6	AR106016	20	6	AR106016	AR106016 Sequence
c 44	11.8	65.6	20	6	AR153357	20	6	AR153357	AR153357 Sequence
c 45	11.8	65.6	21	6	AR139560	21	6	AR139560	AR139560 Sequence

ALIGNMENTS

RESULT 1	I33924	Sequence 2 from patent US 5593974.	18 bp	DNA	Linear	PAT 06-FEB-1997
I33924	I33924	I33924	I33924	I33924	I33924	I33924
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DEFINITION	Sequence 2 from patent US 5593974.	18 bp	DNA	Linear	PAT 06-FEB-1997	
ACCESSION	I33924	I33924	I33924	I33924	I33924	I33924
VERSION	I33924.1	GI:1824715				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 18)					
AUTHORS	Rosenberg, R.D., Simons, M., Edelman, E., Langer, R.S. and DeKeyser, J.-L.					
TITLE	Localized oligonucleotide therapy					
JOURNAL	Patent: US 5593974-A 2 14-JAN-1997;					
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Best Local Similarity 100.0%; Pred. No. 78;
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Db 1 CATGCTCCACCTTGA 18

RESULT 2
A76106

LOCUS A76106 33 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 45 from Patent WO9320210.
ACCESSION A76106
VERSION A76106.1 GI:6088247
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Taylor, G. and Stott, E. J.
TITLE ANTIBODIES FOR TREATMENT AND PREVENTION OF RESPIRATORY SYNCYTIAL
JOURNAL VIRUS INFECTION
Patent: WO 9320210-A 45 14-OCT-1993;
SCOTGEN LTD (GB); TAYLOR GERALDINE (GB)
FEATURES
source 1..33
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 7 a 13 c 5 g 8 t
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttgg 17
|||||
Db 16 CATGGCCACCACTTGG 32

RESULT 3
I68632/c

LOCUS I68632 41 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 5 from patent US 5677124.
ACCESSION I68632
VERSION I68632.1 GI:2830754
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 41)
AUTHORS DuBois, D. B., Winkler, M. M. and Pasloske, B. L.
TITLE Ribonuclease resistant viral RNA standards
JOURNAL Patent: US 5677124-A 5 14-OCT-1997;
FEATURES
source 1..41
Location/Qualifiers
/organism="unknown"

BASE COUNT 15 a 7 c 10 g 9 t
ORIGIN

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Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccaccttga 18
|||||
Db 24 ATGCTCCCACTTAGA 8

RESULT 4
AR014169/c

LOCUS AR014169 33 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 12 from patent US 5773253.
ACCESSION AR014169
VERSION AR014169.1 GI:3971623
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Lineley, P. S., Ledbetter, J. A. and Peach, R.
TITLE MYPPIY variants of CTL A4 and uses thereof
JOURNAL Patent: US 5773253-A 12 30-JUN-1998;
FEATURES
source 1..33
Location/Qualifiers
/organism="unknown"

BASE COUNT 7 a 11 c 8 g 7 t
ORIGIN

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Best Local Similarity 83.3%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
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Db 18 CATGAGCTCCACCTTGA 1

RESULT 5
AX069513

LOCUS AX069513 36 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 177 from Patent WO0102600.
ACCESSION AX069513
VERSION AX069513.1 GI:12579298
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequence.

REFERENCE 1 (bases 1 to 36)
AUTHORS Yuan, C. S.
TITLE Detection of analytes using attenuated enzymes
JOURNAL Patent: WO 0102600-A 177 11-JAN-2001;
GENERAL ATOMICS (US)
FEATURES
Location/Qualifiers
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/note="Oligonucleotides for producing SAH hydrolase mutants"

BASE COUNT 8 a 15 c 7 g 6 t
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Best Local Similarity 83.3%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 18 CATCTCTCCACCCAGGA 35

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LOCUS AX069514 36 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 178 from Patent WO0102600.
ACCESSION AX069514
VERSION AX069514.1 GI:12579299
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequence.

REFERENCE 1 (bases 1 to 36)

AUTHORS Yuan,C.S.
 TITLE Detection of analytes using attenuated enzymes
 JOURNAL Patent: WO 0102600-A 178 11-JAN-2001;
 GENERAL ATOMICS (US)

FEATURES
 source
 1..36
 Location/Qualifiers

/organism="synthetic construct"
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 /note="Oligonucleotides for producing SAH hydrolase mutants"

BASE COUNT 6 a 7 c 15 g 8 t
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Query Match 73.3%; Score 13.2; DB 6; Length 36;
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 19 CATCTCTCCACCCAGGA 2

RESULT 7
 AB068808/c

LOCUS AB068808 20 bp DNA linear SYN 08-AUG-2001
 DEFINITION Synthetic construct DNA, forward primer for human STS sts-IB3268 at lp36.

ACCESSION AB068808
 VERSION AB068808.1 GI:15129612

KEYWORDS
 SOURCE synthetic construct DNA.

ORGANISM
 source synthetic construct
 artificial sequence.

REFERENCE 1 (bases 1 to 20)

AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
 Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
 Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
 and Soeda,E.

TITLE A bac-based sts-content map spanning a 35-mb region of human

chromosome lp35-p36

Genomics. 74 (1), 55-70 (2001)

JOURNAL 21269192

MEDLINE 2 (bases 1 to 20)

REFERENCE Horii,A.

AUTHORS Direct Submission

TITLE Submitted (04-AUG-2001) Akira Horii, Tohoku University School of

Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,

Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
 Tel:81-22-717-8042, Fax:81-22-717-8047)

JOURNAL

FEATURES Location/Qualifiers

source 1..20

/organism="synthetic construct"

/db_xref="taxon:32630"

misc_feature 1..20

/note="forward primer for human STS sts-IB3268 at lp36

sts-IB3268 obtained from clones B13D23, B54F24, B31LL3,
 B375N12, B99F6, B99C7, Human BAC library RPCI-11"

BASE COUNT 5 a 3 c 9 g 3 t

ORIGIN

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Best Local Similarity 87.5%; Pred. No. 4.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgtctccacaccttgg 18

||||| | |||||

Db 18 TGTCCCTACCTTGG 3

RESULT 8
 AX002948/c

LOCUS AX002948 23 bp DNA linear PAT 24-AUG-2000
 DEFINITION Sequence 1 from Patent EP0943678.
 ACCESSION AX002948
 VERSION AX002948.1 GI:9926852

KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequence.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Matsui,T. and Fukuyama,S.
 TITLE Lipase variants

JOURNAL Patent: EP 0943678-A 1 22-SEP-1999;
 NOVONORDISK AS (DK)

FEATURES Location/Qualifiers

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/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Primer 2640"

BASE COUNT 6 a 5 c 9 g 3 t

ORIGIN

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Best Local Similarity 87.5%; Pred. No. 4.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacaccttgg 17

||| ||||| ||||| |||

Db 21 ATTTCTCCACCTGGG 6

RESULT 9

AX002963/c

LOCUS AX002963 24 bp DNA linear PAT 24-AUG-2000

DEFINITION Sequence 16 from Patent EP0943678.

ACCESSION AX002963

VERSION AX002963.1 GI:9926867

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct

artificial sequence.

REFERENCE 1 (bases 1 to 24)

AUTHORS Matsui,T. and Fukuyama,S.

TITLE Lipase variants

JOURNAL Patent: EP 0943678-A 16 22-SEP-1999;

NOVONORDISK AS (DK)

FEATURES Location/Qualifiers

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/organism="synthetic construct"

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BASE COUNT 6 a 5 c 9 g 4 t

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Best Local Similarity 87.5%; Pred. No. 4.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 21 ATTTCTCCACCTGGG 6

RESULT 10

HSA270350

LOCUS HSA270350 24 bp DNA linear PRI 26-JUL-2000

DEFINITION Homo sapiens EMX1 antisense primer.

ACCESSION AJ270350

VERSION AJ270350.1 GI:9557925

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS Palm,K., Salin-Nordstrom,T., Levesque,M.F. and Neuman,T.
TITLE Fetal and adult human CNS stem cells have similar molecular characteristics and developmental potential
JOURNAL Brain Res. Mol. Brain Res. 78 (1-2), 192-195 (2000)
MEDLINE 20351569
REFERENCE 2 (bases 1 to 24)
AUTHORS Palm,K.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1999) Surgery, Cedars Sinai Medical Center, 8700 Beverly Blvd., Los Angeles, CA 90048, US
COMMENT Related entry: X68879.
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/db_xref="taxon:9606"
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 2 ATGTCCTCCCATTTGG 17
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LOCUS AR090768 28 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 888 from patent US 5994076.
ACCESSION AR090768
VERSION AR090768.1 GI:10017523
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 888 30-NOV-1999;
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BASE COUNT 10 a 6 c 8 g 4 t
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Db 26 TGTCGTCATCTTGA 11
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AX350231/c
LOCUS AX350231 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 48 from Patent WO0200884.
ACCESSION AX350231
VERSION AX350231.1 GI:18615899
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.

1 (sites)
AUTHORS Galarza,J.M. and Latham,T.E.
TITLE Nucleotide sequence of influenza A/udorn/72 (h3n2) genome
JOURNAL Patent: WO 0200884-A 48 03-JAN-2002;
AMERICAN CYANAMID COMPANY (US)
FEATURES
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/note="Primer"
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Best Local Similarity 87.5%; Pred. No. 4.3e+04;
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Db 25 CATGGCCTCCCATG 10
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A84409
LOCUS A84409 33 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 24 from Patent WO9845704.
ACCESSION A84409
VERSION A84409.1 GI:6733328
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Tullin,S. and Kasper,A.
TITLE A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN INFLUENCE ON A CELLULAR RESPONSE
JOURNAL Patent: WO 9845704-A 24 15-OCT-1998;
TULLIN SOEREN (DK); KASPER ALMHOLT (DK)
FEATURES
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BASE COUNT 6 a 10 c 6 g 11 t
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E11199
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XX E11199;
AC E11199;
XX E11199.1
XX E11199.1
DT 08-OCT-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
DE Probe.
XX JP 1996089300-A/14.
XX unidentified
OC unclassified.

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Job time: 8894 sec

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XX [1]
RN 1-35
RA Tokuda C., Fukuda T., Saito I.;
RT "METHOD FOR DETECTING NUCLEIC ACID";
RL Patent number JP1996089300-A/14, 09-APR-1996.
RL MITSUI TOAISU CHEM INC, MITSUI PHARMACEUT INC.
XX

CC OS None
CC OC Artificial sequences.
CC PN JP 1996089300-A/14
CC PD 09-APR-1996
CC PF 28-SEP-1994 JP 1994232637
CC PI TOKUDA CHIKASHI, FUKUDA TAMOTSU, SAITO IZUMI
CC PC C12Q1/68,G01N33/58//C12N15/09,C12Q1/70;
CC CC strandedness: Single;
CC CC topology: Linear;
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Best Local Similarity 87.5%; Pred. No. 4.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 16 CACGTCTCTCCACCTCG 31

RESULT 15
AX223672/c
LOCUS AX223672 48 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 9114 from Patent WO0159103.
ACCESSION AX223672
VERSION AX223672.1 GI:15551396
KEYWORDS
SOURCE synthetic construct.
ORGANISM -synthetic construct
artificial sequence.
REFERENCE
1 (bases 1 to 48)
Blatt,L., McSwiggen,J. and Chowrira,B.M.
METHOD and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 9114 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 16 TTTCCTCGCCTTGA 1
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:31 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-6
Perfect score: 18
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Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	16	US-09-241-561-6	Sequence 6, Appli
2	14.8	82.2	30	8	US-08-465-971A-5	Sequence 5, Appli
3	14.8	82.2	30	8	US-08-465-971A-9	Sequence 9, Appli
4	14.8	82.2	30	16	US-09-228-420-5	Sequence 5, Appli
5	14.8	82.2	30	16	US-09-228-420-9	Sequence 9, Appli
6	14.8	82.2	30	37	US-10-006-394-5	Sequence 5, Appli
7	14.8	82.2	30	37	US-10-006-394-9	Sequence 9, Appli
8	14.8	82.2	34	8	US-08-465-971A-7	Sequence 7, Appli
9	14.8	82.2	34	16	US-09-228-420-7	Sequence 7, Appli
10	14.8	82.2	34	37	US-10-006-394-7	Sequence 7, Appli
11	14.8	82.2	36	17	US-09-338-248-101	Sequence 101, App
12	14.4	80.0	25	35	US-09-956-584-422010	Sequence 422010, Sequence 427909,
13	14.4	80.0	25	62	US-60-234-017-427909	Sequence 427909,
14	14.4	80.0	48	37	US-10-017-974-25182	Sequence 25182, A
15	13.8	76.7	25	34	US-09-922-181A-478	Sequence 478, App
16	13.8	76.7	25	34	US-09-922-181A-1975	Sequence 1975, Ap
17	13.8	76.7	25	34	US-09-922-181A-1976	Sequence 1976, Ap
18	13.8	76.7	25	34	US-09-922-181A-1977	Sequence 1977, Ap
19	13.8	76.7	25	34	US-09-922-181A-1978	Sequence 1978, Ap
20	13.8	76.7	25	34	US-09-922-181A-1979	Sequence 1979, Ap
21	13.8	76.7	25	34	US-09-922-181A-1980	Sequence 1980, Ap
22	13.8	76.7	25	34	US-09-922-181A-1981	Sequence 1981, Ap
23	13.8	76.7	25	34	US-09-922-181A-1982	Sequence 1982, Ap
24	13.8	76.7	25	34	US-09-922-181A-1983	Sequence 1983, Ap
25	13.8	76.7	25	35	US-09-956-584-103083	Sequence 103083,
26	13.8	76.7	25	35	US-09-956-584-309394	Sequence 309394,
27	13.8	76.7	25	62	US-60-234-017-82282	Sequence 82282, A
28	13.8	76.7	25	62	US-60-234-017-281428	Sequence 281428,
29	13.8	76.7	33	7	US-08-313-311B-45	Sequence 45, Appli
30	13.8	76.7	41	12	US-08-841-251-5	Sequence 5, Appli
31	13.8	76.7	41	26	US-09-665-638-5	Sequence 5, Appli

c 32 13.4 74.4 23 1 PCT-US00-1909A-388 Sequence 388, App
c 33 13.4 74.4 23 37 US-10-010-802-388 Sequence 388, App
c 34 13.4 74.4 25 74 US-60-353-987-79860 Sequence 79860, A
c 35 13.4 74.4 25 74 US-60-353-987-280884 Sequence 280884
c 36 13.4 74.4 48 31 US-09-827-395A-2496 Sequence 2496, Ap
c 37 13.2 73.3 20 14 US-09-071-699-20 Sequence 20, Appl
c 38 13.2 73.3 20 17 US-09-303-040-20 Sequence 20, Appl
c 39 13.2 73.3 20 17 US-09-303-040-20 Sequence 20, Appl
c 40 13.2 73.3 24 1 PCT-US00-24784-160 Sequence 160, App
c 41 13.2 73.3 24 1 PCT-US00-24784-182 Sequence 182, App
c 42 13.2 73.3 25 35 US-09-956-584-146730 Sequence 146730, App
c 43 13.2 73.3 25 35 US-09-956-584-158941 Sequence 158941, App
c 44 13.2 73.3 25 35 US-09-956-584-260346 Sequence 260346, App
c 45 13.2 73.3 25 35 US-09-956-584-391677 Sequence 391677, App

ALIGNMENTS

RESULT 1
US-09-241-561-6
; Sequence 6, Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12534.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-6

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccaccttggg 18
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Db 1 catgtctccaccttggg 18

RESULT 2
US-08-465-971A-5
; Sequence 5, Application US/08465971A
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,971A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-465-971A-5

Query Match 82.2%; Score 14.8; DB 8; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttggg 18
|||||
Db 12 CATGAATCCACCTTGGG 29

RESULT 3
US-08-465-971A-9
; Sequence 9, Application US/08465971A
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,971A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-465-971A-9

Query Match 82.2%; Score 14.8; DB 8; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
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Db 12 CATGAACCTCCACCTTGA 29

RESULT 4
US-09-228-420-5
; Sequence 5, Application US/09228420
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,971
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-228-420-5

Query Match 82.2%; Score 14.8; DB 16; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
||||| ||||| ||||| |||||
Db 12 CATGAACCTCCACCTTGA 29

RESULT 5
US-09-228-420-9
; Sequence 9, Application US/09228420
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/006,394
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,420
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073

STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/228,420
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,971
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-228-420-9

Query Match 82.2%; Score 14.8; DB 16; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
||||| ||||| ||||| |||||
Db 12 CATGAACCTCCACCTTGA 29

RESULT 6
US-10-006-394-5
; Sequence 5, Application US/10006394
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/006,394
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,420
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073

REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-006-394-5

Query Match 82.2%; Score 14.8; DB 37; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
||||| |||||||||
DB 12 CATGAACCTCCACCTTGA 29

RESULT 7

US-10-006-394-9
Sequence 9, Application US/10006394
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/006,394
FILING DATE: 10-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/228,420
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-006-394-9

Query Match 82.2%; Score 14.8; DB 37; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
||||| |||||||||
DB 12 CATGAACCTCCACCTTGA 29

RESULT 8

US-08-465-971A-7
Sequence 7, Application US/08465971A
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-465-971A-7

Query Match 82.2%; Score 14.8; DB 8; Length 34;
Best Local Similarity 88.9%; Pred. No. 7.1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
||||| |||||||||
DB 16 CATGAACCTCCACCTTGA 33

RESULT 9

US-09-228-420-7
Sequence 7, Application US/09228420
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/228,420
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,971
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
US-09-228-420-7

Query Match 82.2%; Score 14.8; DB 16; Length 34;
Best Local Similarity 88.9%; Pred. No. 7.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctctccaccttggga 18
||||| |||||||||
DB 16 CATGAACCTCCACCTTGA 33

RESULT 10
US-10-006-394-7
Sequence 7, Application US/10006394
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cecchi, Byrne, Bain, Gilfillan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/006,394
FILING DATE: 10-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/228,420
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-006-394-7

Query Match 82.2%; Score 14.8; DB 37; Length 34;
Best Local Similarity 88.9%; Pred. No. 7.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctctccaccttggga 18
||||| |||||||||
DB 16 CATGAACCTCCACCTTGA 33

RESULT 11
US-09-338-248-101
Sequence 101, Application US/09338248
GENERAL INFORMATION:
APPLICANT: Lee, Stephen C
TITLE OF INVENTION: Method of Producing Permutins by
Scanning Permutagenesis
FILE REFERENCE: C 3041
CURRENT APPLICATION NUMBER: US/09/338,248
NUMBER OF SEQ ID NOS: 368
CURRENT FILING DATE: 1999-06-22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 101
LENGTH: 36
TYPE: DNA
ORGANISM: Synthetic
US-09-338-248-101

Query Match 82.2%; Score 14.8; DB 17; Length 36;
Best Local Similarity 88.9%; Pred. No. 7.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctctccaccttggga 18
||||| |||||||||
DB 9 catgtctctccaccttggga 26

RESULT 12
US-09-956-584-422010/c
Sequence 422010, Application US/09956584
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
FILE REFERENCE: 3115.1
CURRENT APPLICATION NUMBER: US/09/956,584
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,017
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 422010
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-956-584-422010

Query Match 80.0%; Score 14.4; DB 35; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgtctctccaccttggga 18
||||| |||||||||
DB 17 TGTACTCCACCTTGA 2

```
RESULT 13
US-60-234-017-427909/c
; Sequence 427909, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mitmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 427909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV145609
US-60-234-017-427909

Query Match      80.0%; Score 14.4; DB 62; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgtctccacacttggg 18
Db 17 TGTACTCCACCTTGGG 2

RESULT 14
US-10-017-974-25182/c
; Sequence 25182, Application US/10017974
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Lawrence
; TITLE OF INVENTION: Nucleic Acid-Based Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Nile Virus Infection
; FILE REFERENCE: MH800,1109-A (400/037)
; CURRENT APPLICATION NUMBER: US/10/017,974
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 37080
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25182
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-017-974-25182

Query Match      80.0%; Score 14.4; DB 37; Length 48;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgtctccacacttggg 18
Db 16 TTTCTCCACCTTGGG 1

RESULT 15
US-09-922-181A-478/c
; Sequence 478, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
```

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; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 478
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-478

Query Match      76.7%; Score 13.8; DB 34; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacacttgg 17
Db 17 CAGGTCTCCACCATGG 1

Search completed: October 12, 2002, 20:42:32
Job time: 16402 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:31 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-6
Perfect score: 18
Sequence: 1 catgtctccaccttga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-6
2	14.4	80.0	48	7	US-10-156-306-4143
3	13.8	76.7	30	1	PCT-US02-25943-54675
4	13.8	76.7	41	7	US-10-120-013-5
5	13.4	74.4	23	7	US-10-009-678-388
6	13.2	73.3	20	1	PCT-US02-25943-28430
7	13.2	73.3	35	1	PCT-US02-25943-28431
8	13	72.2	15	1	PCT-US02-25943-62053
9	13	72.2	17	1	PCT-US02-25943-62054
10	13	72.2	19	1	PCT-US02-25943-24151
11	13	72.2	49	1	PCT-US02-25943-24149
12	12.8	71.1	25	5	US-09-992-665-105
13	12.8	71.1	24	5	US-09-396-1966-1664
14	12.8	71.1	25	5	US-09-396-1966-24560
15	12.8	71.1	25	5	US-09-396-1966-35757
16	12.8	71.1	25	5	US-09-396-1966-53939
17	12.8	71.1	28	5	US-09-225-2018-888
18	12.8	71.1	33	5	US-09-417-197-24
19	12.8	71.1	33	6	US-10-072-036-24
20	12.8	71.1	45	6	US-10-012-064-168
21	12.8	71.1	45	6	US-10-013-913A-168
22	12.8	71.1	45	6	US-10-015-385A-168
23	12.8	71.1	45	6	US-10-015-388A-168
24	12.8	71.1	45	6	US-10-015-390A-168
25	12.8	71.1	45	6	US-10-011-692A-168

26	12.8	71.1	45	6	US-10-011-795A-168	Sequence 168, App
27	12.8	71.1	45	6	US-10-012-101B-168	Sequence 168, App
28	12.8	71.1	45	6	US-10-012-753A-168	Sequence 168, App
29	12.8	71.1	45	6	US-10-015-395A-168	Sequence 168, App
30	12.8	71.1	45	6	US-10-006-746A-168	Sequence 168, App
31	12.8	71.1	45	6	US-10-011-795B-168	Sequence 168, App
32	12.8	71.1	45	6	US-10-012-064A-168	Sequence 168, App
33	12.8	71.1	45	6	US-10-012-064-168	Sequence 168, App
34	12.8	71.1	45	6	US-10-020-063A-168	Sequence 168, App
35	12.8	71.1	45	7	US-10-006-063A-168	Sequence 168, App
36	12.8	71.1	45	7	US-10-006-117A-168	Sequence 168, App
37	12.8	71.1	45	7	US-10-006-130A-168	Sequence 168, App
38	12.8	71.1	45	7	US-10-006-172A-168	Sequence 168, App
39	12.8	71.1	45	7	US-10-006-768A-168	Sequence 168, App
40	12.8	71.1	45	7	US-10-017-527A-168	Sequence 168, App
41	12.8	71.1	45	7	US-10-017-610A-168	Sequence 168, App
42	12.8	71.1	45	7	US-10-006-041A-168	Sequence 168, App
43	12.8	71.1	45	7	US-10-006-818A-168	Sequence 168, App
44	12.8	71.1	45	7	US-10-012-121A-168	Sequence 168, App
45	12.8	71.1	45	7	US-10-015-386A-168	Sequence 168, App

ALIGNMENTS

RESULT 1
US-09-945-131-6
; Sequence 6, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-6

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
| | | | | | | | | | | | | | | | | |
Db 1 catgtctccaccttga 18

RESULT 2
US-10-156-306-4143/c
; Sequence 4143, Application US/10156306
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)

;; CURRENT APPLICATION NUMBER: US/10/156,306
;; CURRENT FILING DATE: 2002-05-28
;; NUMBER OF SEQ ID NOS: 8013
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 4143
;; LENGTH: 48
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306-4143

Query Match 80.0%; Score 14.4; DB 7; Length 48;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgtctccacccttggg 18
Db 16 TTCTCTCCACCTTGA 1
| | | | | | | | | | | | | | | | | | | | | |

RESULT 3
PCT-US02-25943-54675
;; Sequence 54675, Application PC/TUS0225943
;; GENERAL INFORMATION:
;; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
;; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
;; CURRENT APPLICATION NUMBER: PCT/US02/25943
;; CURRENT FILING DATE: 2002-08-27
;; NUMBER OF SEQ ID NOS: 64158
;; SOFTWARE: Proprietary
;; SEQ ID NO 54675
;; LENGTH: 30
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
;; FEATURE:
;; LOCATION: (5356688)...(5356717)
;; OTHER INFORMATION: Chromosome - 1 Strand - positive ConnectronObjectNumber = 58582
PCT-US02-25943-54675

Query Match 76.7%; Score 13.8; DB 1; Length 30;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacccttgg 17
Db 6 catgtccaccaccctgg 22
| | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-10-120-013-5/c
;; Sequence 5, Application US/10120013
;; GENERAL INFORMATION:
;; APPLICANT: Pasloske, Brittan L.
;; Brown, David
;; Dubois, Dwight
;; Winkler, Matthew
;; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
AND UTILIZATION
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/120,013
;; FILING DATE: 10-Apr-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/881,571
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/675,153
;; FILING DATE: 03-JUL-1996
;; APPLICATION NUMBER: US 60/021,145
;; FILING DATE: 03-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: AMBI:033
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7577
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 41 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-120-013-5

Query Match 76.7%; Score 13.8; DB 7; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacccttggg 18
Db 24 ATGTCTCCCAACTTAGA 8
| | | | | | | | | | | | | | | | | | | | | |

RESULT 5
US-10-009-678-388/c
;; Sequence 388, Application US/10009678
;; GENERAL INFORMATION:
;; APPLICANT: Genaisance Pharmaceuticals
;; APPLICANT: Denton, R. Rex
;; APPLICANT: Nandabalan, Krishnan
;; APPLICANT: Chew, Anne
;; APPLICANT: Stephens, J. Claiborne
;; APPLICANT: Duda, Amy
;; APPLICANT: Windemuth, Andreas
;; TITLE OF INVENTION: Drug Target Isoenes: polymorphisms in the Interleukin
;; TITLE OF INVENTION: 4 Receptor Alpha Gene
;; FILE REFERENCE: MNH-0002 PCT IL4R alpha
;; CURRENT APPLICATION NUMBER: US/10/009,678
;; CURRENT FILING DATE: 2002-04-04
;; PRIOR APPLICATION NUMBER: 60/143,435
;; PRIOR FILING DATE: 1999-07-13
;; NUMBER OF SEQ ID NOS: 413
;; SOFTWARE: PatentIn ver. 2.1
;; SEQ ID NO 388
;; LENGTH: 23
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-009-678-388

Query Match 74.4%; Score 13.4; DB 7; Length 23;
Best Local Similarity 93.3%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 catgtctccaccctt 15
Db 16 CATGTCTCTACCTT 2
| | | | | | | | | | | | | | | | | | | | | |

```
RESULT 6
PCT-US02-25943-28430
; Sequence 28430, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 28430
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2751880)...(2751900)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 30446
PCT-US02-25943-28430

Query Match 73.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
   ||| ||| ||| ||| |||
Db 1 catctccaccacctggga 18

RESULT 7
PCT-US02-25943-28431
; Sequence 28431, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 28431
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2751880)...(2751915)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 30447
PCT-US02-25943-28431

Query Match 73.3%; Score 13.2; DB 1; Length 35;
Best Local Similarity 83.3%; Pred. No. 7.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
   ||| ||| ||| ||| |||
Db 16 catctccaccacctggga 33

RESULT 8
PCT-US02-25943-62053/c
; Sequence 62053, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62053
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6059906)...(6059920)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 66
PCT-US02-25943-62053

Query Match 72.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccacc 13
   ||| ||| ||| ||| |||
Db 15 CATGTCTCTCCACC 3

RESULT 9
PCT-US02-25943-62054
; Sequence 62054, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62054
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6059906)...(6059922)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 66
PCT-US02-25943-62054

Query Match 72.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccacc 13
   ||| ||| ||| ||| |||
Db 1 catgtctccacc 13

RESULT 10
PCT-US02-25943-24151
; Sequence 24151, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 24151
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2365668)...(2365686)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 25
PCT-US02-25943-24151

Query Match 72.2%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 catgtctccacc 13
|||||
Db 1 catgtctccacc 13

RESULT 11
PCT-US02-25943-24149/c
; Sequence 24149, Application PCTUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 24149
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2365638)...(2365686)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 25934
PCT-US02-25943-24149

Query Match 72.2%; Score 13; DB 1; Length 49;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccacc 13
|||||
Db 49 CATGCTCCACC 37

RESULT 12
US-09-992-665-105
; Sequence 105, Application US/09992665
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-105

Query Match 71.1%; Score 12.8; DB 5; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccaccctgg 17
|||||
Db 2 atgtctccaccctgg 17

RESULT 13
US-09-396-196G-1664/c
; Sequence 1664, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1664

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccaccctgg 17
|||||
Db 23 ATGTACTGCACCTTG 8

RESULT 14
US-09-396-196G-24560
; Sequence 24560, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24560

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccctgg 16
|||||
Db 10 caggctctccagcttg 25

RESULT 15
US-09-396-196G-35757/c
; Sequence 35757, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35757
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-35757

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtcctccaccttg 16
||| ||||| |||||
Db 25 CAAGTCCTGCACCTTG 10

Search completed: October 12, 2002, 17:27:31
Job time: 10806 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:31 ; Search time 1154.93 seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-7
Perfect score: 18
Sequence: 1 gatcaggcgtgcctcaaa 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	18	100.0	18	5	US-09-945-131-7		Sequence 7, Appli
2	12.8	71.1	50	6	US-10-131-831-7370		Sequence 7370, Ap
3	12.8	71.1	50	6	US-10-131-827-7370		Sequence 7370, Ap
4	12.4	68.9	25	5	US-09-396-196G-1134		Sequence 1134, Ap
5	12.4	68.9	25	5	US-09-396-196G-32558		Sequence 32558, A
6	12.4	68.9	38	7	US-10-000-467-4		Sequence 4, Appli
7	12.4	68.9	39	7	US-10-000-467-3		Sequence 3, Appli
8	12.2	67.8	21	1	PCT-US02-25943-60781		Sequence 60781, A
9	12.2	67.8	25	5	US-09-992-665-206		Sequence 206, App
10	12.2	67.8	25	5	US-09-396-196G-1135		Sequence 1135, Ap
11	12.2	67.8	25	5	US-09-396-196G-25470		Sequence 25470, A
12	12.2	67.8	25	5	US-09-396-196G-25471		Sequence 25471, A
13	12.2	67.8	25	5	US-09-396-196G-52771		Sequence 52771, A
14	12.2	67.8	25	5	US-09-396-196G-68382		Sequence 68382, A
15	12.2	67.8	29	5	US-09-426-776A-2		Sequence 2, Appli
16	12.2	67.8	35	1	PCT-US02-25943-52461		Sequence 52461, A
17	12.2	67.8	38	1	PCT-US02-25943-57045		Sequence 57045, A
18	12.2	67.8	50	5	US-09-709-201B-29		Sequence 29, Appl
19	11.8	65.6	17	7	US-10-156-306-5152		Sequence 5152, Ap
20	11.8	65.6	17	7	US-10-156-306-5992		Sequence 5992, Ap
21	11.8	65.6	25	5	US-09-956-604-55880		Sequence 55880, A
22	11.8	65.6	25	5	US-09-956-604-55913		Sequence 55913, A
23	11.8	65.6	25	5	US-09-396-196G-73		Sequence 73, Appl
24	11.8	65.6	25	5	US-09-396-196G-37713		Sequence 37713, A
25	11.8	65.6	25	5	US-09-396-196G-37714		Sequence 37714, A

ALIGNMENTS

RESULT 1

US-09-945-131-7
; Sequence 7, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-7

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gatcaggcgtgcctcaaa 18
Db 1 gatcaggcgtgcctcaaa 18

RESULT 2

US-10-131-831-7370
; Sequence 7370, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING

; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131.831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7370
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-7370

Query Match 71.1%; Score 12.8; DB 6; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tcaggcgtgcctcaaa 18
| | | | | | | | | | | | | | | | | |
Db 11 taaggcctgcctcaaa 26

RESULT 3
US-10-131-827-7370
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131.827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7370
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-7370

Query Match 71.1%; Score 12.8; DB 6; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tcaggcgtgcctcaaa 18
| | | | | | | | | | | | | | | | | |
Db 11 taaggcctgcctcaaa 26

RESULT 4
US-09-396-196G-1134
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1134

Query Match 68.9%; Score 12.4; DB 5; Length 25;
Best Local Similarity 92.9%; Pred. No. 4.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcct 14
| | | | | | | | | | | | | |
Db 12 gatcaggcgtgcct 25

RESULT 5
US-09-396-196G-32558/c
; Sequence 32558, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-32558

Query Match 68.9%; Score 12.4; DB 5; Length 25;
Best Local Similarity 92.9%; Pred. No. 4.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 aggcgtgcctcaaa 18
| | | | | | | | | | | | | |
Db 23 AGCGGTGACTCAA 10

RESULT 6
US-10-000-467-4
; Sequence 4, Application US/10000467
; GENERAL INFORMATION:
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Tabone, John C.
; APPLICANT: Howbert, J. Jeffrey
; APPLICANT: Mulligan, John T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; FILE REFERENCE: 780068.418C3
; CURRENT APPLICATION NUMBER: US/10/000,467
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide sequence which is linked to a

; OTHER INFORMATION: nylon bead
US-10-000-467-4

Query Match 68.9%; Score 12.4; DB 7; Length 38;
Best Local Similarity 92.9%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatcaggcgctgcct 14
| | | | | | | | | | | | | | | |
Db 7 gatcaggcgcgctct 20

RESULT 7
US-10-000-467-3
; Sequence 3, Application US/10000467
; GENERAL INFORMATION:
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Tabone, John C.
; APPLICANT: Howbert, J. Jeffrey
; APPLICANT: Mulligan, John T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; TITLE OF INVENTION: SENSITIVITY IN THE ANALYSIS OF BIOLOGICAL-BASED ASSAYS
; FILE REFERENCE: 780068.418C3
; CURRENT APPLICATION NUMBER: US/10/000,467
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide DMO 596
US-10-000-467-3

Query Match 68.9%; Score 12.4; DB 7; Length 39;
Best Local Similarity 92.9%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatcaggcgctgcct 14
| | | | | | | | | | | | | | | |
Db 7 gatcaggcgcgctct 20

RESULT 8
PCT-US02-25943-60781/c
; Sequence 60781, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 60781
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5924871)...(5924891)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 65096
PCT-US02-25943-60781

Query Match 67.8%; Score 12.2; DB 1; Length 21;
Best Local Similarity 82.4%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gatcaggcgctgcctcaa 17
| | | | | | | | | | | | | | | |

Db 18 GGTCAGGCGCGCCTCGA 2

RESULT 9
US-09-992-665-206
; Sequence 206, Application US/09992665
; GENERAL INFORMATION:
; APPLICANT: Kala Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-206

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atcaggcgctgcctcaaa 18
| | | | | | | | | | | | | | | |
Db 6 aactggcgctgcctctaa 22

RESULT 10
US-09-396-196G-1135
; Sequence 1135, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1135
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1135

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atcaggcgctgcctcaaa 18
| | | | | | | | | | | | | | | |
Db 1 atcaggagtgctctacaa 17

RESULT 11
US-09-396-196G-25470
; Sequence 25470, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack

; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-25470

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atcaggcgtgcctcaaa 18
||||| |||||||
Db 7 atcaggagtaccctcaca 23

RESULT 12
US-09-396-196G-25471
; Sequence 25471, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-25471

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atcaggcgtgcctcaaa 18
||||| |||||||
Db 1 atcaggagtaccctcaca 17

RESULT 13
US-09-396-196G-52771/c
; Sequence 52771, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52771
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52771

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaa 17
||||| |||||||
Db 19 GATCAGGAGAGCATCAA 3

RESULT 14
US-09-396-196G-68382/c
; Sequence 68382, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68382
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-68382

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atcaggcgtgcctcaaa 18
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Db 21 ATCAGGAGTACTGAAA 5

RESULT 15
US-09-426-776A-2
; Sequence 2, Application US/09426776A
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: TAN, Nguan Soon
; APPLICANT: HO, Bow
; APPLICANT: LAM, Toong Jin
; TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS ENCODING A SECRETORY SIGNAL FOR EXPRESS
; TITLE OF INVENTION: SECRETION OF HETEROLOGOUS RECOMBINANT PROTEINS
; FILE REFERENCE: 1781-0178P
; CURRENT APPLICATION NUMBER: US/09/426,776A
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chloramphenicol acetyltransferase (CAT) gene forward primer de

US-09-426-776A-2

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 Db 3 atcggccgtgccttaaa 19

Search completed: October 12, 2002, 17:27:32
 Job time: 10807 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: October 12, 2002, 16:51:16 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: us-09-945-131-5
Perfect score: 18
Sequence: 1 ggtcgggtctccggc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: gb_ro.*

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12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

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32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	18	100.0	18	6	A42365	A42365 Sequence 25
	2	18	100.0	18	6	A44383	A44383 Sequence 13
	3	18	100.0	18	6	A47170	A47170 Sequence 13
C	4	18	100.0	18	6	AR098341	AR098341 Sequence
	5	18	100.0	18	6	AR098342	AR098342 Sequence
C	6	18	100.0	18	6	AR141743	AR141743 Sequence
	7	18	100.0	18	6	AR141744	AR141744 Sequence
C	8	18	100.0	18	6	AR146396	AR146396 Sequence
	9	18	100.0	18	6	AR146397	AR146397 Sequence
	10	18	100.0	18	6	AX081380	AX081380 Sequence
	11	18	100.0	18	6	AX104469	AX104469 Sequence
	12	18	100.0	18	6	AX283210	AX283210 Sequence
	13	18	100.0	18	6	AX283279	AX283279 Sequence
	14	18	100.0	18	6	AX355446	AX355446 Sequence
	15	18	100.0	18	6	BD005488	BD005488 Catlonic
	16	18	100.0	18	6	I33923	I33923 Sequence 1
	17	18	100.0	18	6	I56531	I56531 Sequence 6
C	18	100.0	18	6	I56532	I56532 Sequence 7	
	19	18	100.0	18	6	I70385	I70385 Sequence 1
	20	16.4	91.1	18	6	AX104436	AX104436 Sequence
	21	16.4	91.1	18	6	AX104470	AX104470 Sequence
	22	16.4	91.1	18	6	AX355440	AX355440 Sequence
	23	16.4	91.1	18	6	AX355441	AX355441 Sequence
	24	14.8	82.2	18	6	A40324	A40324 Sequence 15
	25	14.8	82.2	18	6	A42350	A42350 Sequence 10
	26	14.8	82.2	18	6	A4382	A4382 Sequence 12
	27	14.8	82.2	18	6	A47169	A47169 Sequence 12
	28	14.8	82.2	18	6	A56644	A56644 Sequence 11
	29	14.8	82.2	18	6	A80365	A80365 Sequence 11
	30	14.8	82.2	18	6	AR091660	AR091660 Sequence
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	32	14.8	82.2	18	6	AR123437	AR123437 Sequence
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	34	14.8	82.2	18	6	AR167441	AR167441 Sequence
	35	14.8	82.2	18	6	AX081343	AX081343 Sequence
	36	14.8	82.2	18	6	AX283173	AX283173 Sequence
	37	14.8	82.2	18	6	AX283239	AX283239 Sequence
	38	14.8	82.2	18	6	E05310	E05310 Anti-sense
	39	14.8	82.2	18	6	I33926	I33926 Sequence 4
	40	14.8	82.2	18	6	I84723	I84723 Sequence 11
	41	14.8	82.2	19	6	AR144059	AR144059 Sequence
	42	14.8	82.2	24	6	AR006742	AR006742 Sequence
	43	14.8	82.2	24	6	AR065943	AR065943 Sequence
	44	14.8	82.2	24	6	AR116413	AR116413 Sequence
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ALIGNMENTS

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A42365		A42365	Sequence 25 from Patent WO9501363.				
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DEFINITION		A42365	Sequence 25 from Patent WO9501363.				
ACCESSION		A42365	Sequence 25 from Patent WO9501363.				
VERSION		A42365.1	GI:2297841				
KEYWORDS							
SOURCE			unidentified.				
ORGANISM			unclassified.				
REFERENCE			1 (bases 1 to 18)				
AUTHORS			Uhlmann,E and Meier,C.				
TITLE			METHYLPHOSPHONIC ACID ESTER, PROCESS FOR PREPARING THE SAME AND ITS				
JOURNAL			US				
COMMENT			Patent: WO 9501363-A 25 12-JAN-1995;				
			HOECHST AG (DE)				
			Other publication FI 956341 960219				
			Other publication CA 2165971 950112				
			Other publication NO 955352 960214				
			Other publication AU 7073594 950124				
			Other publication DE 4321946 950112.				
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
Db 1 GTGTCTGGGGGTCTCCGGGC 18

RESULT 6
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LOCUS      ARI14743      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6147123.
ACCESSION  ARI14743
VERSION     ARI14743.1 GI:15101259
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Chojkier,M. and Carson,D.
TITLE       Treatment and prevention of hepatic disorders
JOURNAL     Patent: US 6147123-A 3 14-NOV-2000;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
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LOCUS      ARI146397      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6218437.
ACCESSION  ARI146397
VERSION     ARI146397.1 GI:15109586
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Chojkier,M.
TITLE       Treatment and prevention of hepatic disorders
JOURNAL     Patent: US 6218437-A 4 17-APR-2001;
FEATURES    Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTCTGGGGGTCTCCGGGC 18

RESULT 10
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LOCUS      AX081380      18 bp      DNA      linear      PAT 27-FEB-2001
DEFINITION Sequence 59 from Patent WO0108707.
ACCESSION  AX081380
VERSION     AX081380.1 GI:13170222
KEYWORDS    .
SOURCE      synthetic construct.
ORGANISM    synthetic construct
             artificial sequence.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
TITLE       Conjugates and methods for the production thereof, and their use
             for transporting molecules via biological membranes
JOURNAL     Patent: WO 0108707-A 59 08-FEB-2001;
FEATURES    Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
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RESULT 7
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LOCUS      ARI14744      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6147123.
ACCESSION  ARI14744
VERSION     ARI14744.1 GI:15101260
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Chojkier,M. and Carson,D.
TITLE       Treatment and prevention of hepatic disorders
JOURNAL     Patent: US 6147123-A 4 14-NOV-2000;
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BASE COUNT  0 a      5 c      9 g      4 t
ORIGIN

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LOCUS      ARI146396      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6218437.
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|||||
Db 1 GTGTCGGGTCCTCCGGC 18

RESULT 11
AX104469
LOCUS AX104469 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 661 from Patent WO0122972.
ACCESSION AX104469
VERSION AX104469.1 GI:13920666
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 18).
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 561 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
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BASE COUNT      0 a      5 c      9 g      4 t
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
AX283210
LOCUS AX283210 18 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 48 from Patent WO0179216.
ACCESSION AX283210
VERSION AX283210.1 GI:17044091
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (sites)
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing them
JOURNAL Patent: WO 0179216-A 48 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
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/organism="synthetic construct"
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
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LOCUS AX283279 18 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 43 from Patent WO0179249.
ACCESSION AX283279
VERSION AX283279.1 GI:17044160
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (sites)
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing the same
JOURNAL Patent: WO 0179249-A 43 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
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LOCUS AX355446 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 474 from Patent WO0197843.
ACCESSION AX355446
VERSION AX355446.1 GI:18620114
KEYWORDS
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ORGANISM
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artificial sequence.
REFERENCE 1 (sites)
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 474 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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RESULT 15
BD005488 18 bp DNA linear PAT 31-JAN-2002
LOCUS Cationic polymer and lipoprotein-containing system for gene
DEFINITION delivery.
ACCESSION BD005488
VERSION BD005488.1 GI:18633859
KEYWORDS JP 2001501812-A/1.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Maruyama,A., Akaike,T. and Kim,S.W.
TITLE Cationic polymer and lipoprotein-containing system for gene
delivery
JOURNAL Patent: JP 2001501812-A 1 13-FEB-2001;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2001501812-A/1
PD 13-FEB-2001
PF 03-JUL-1997 JP 1998504522
PR
PI JIN SEOK KIM,ATSUSHI MARUYAMA,TOSHIHIRO AKAIKE,SUNG WAN KIM PC
C12N15/64

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Job time: 8892 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

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39.012 Million cell updates/sec

Title: US-09-945-131-5

Perfect score: 18

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Searched: 1736436 seqs, 858457221 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AAQ42217	Antisense sequence
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3	18	100.0	18	AAQ37635	Antisense oligonuc
4	18	100.0	18	AAQ44437	Antisense oligonuc
5	18	100.0	18	AAQ88725	Mouse c-myc modifi
6	18	100.0	18	AAQ88725	Multi-G oligonucle
7	18	100.0	18	AAQ17811	Glycosaminoglycan
8	18	100.0	18	AAQ17812	Glycosaminoglycan
9	18	100.0	18	AAQ93470	C-myb antisense ol

10	18	100.0	18	AAQ13831	C-myb phosphorothi
11	18	100.0	18	AAF99482	Immunostimulatory
12	18	100.0	18	AAF60950	Anti-c-myb oligonu
13	18	100.0	18	AAF86998	Rat c-myb phosphor
14	18	100.0	18	AAF86999	Rat c-myb phosphor
15	18	100.0	18	AAH49233	Anti-c-myb oligonu
16	18	100.0	18	ABL01642	c-myb targeted ant
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19	16.4	91.1	18	AAT28317	Multi-G oligonucle
20	16.4	91.1	18	AAF99473	Immunostimulatory
21	16.4	91.1	18	AAF99483	Immunostimulatory
22	16	88.9	17	AAQ87994	Antisense oligonuc
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25	14.8	82.2	18	AAQ31560	c-myb mRNA complem
26	14.8	82.2	18	AAQ42220	Antisense sequence
27	14.8	82.2	18	AAQ35159	Human c-myb antis
28	14.8	82.2	18	AAQ41938	Human c-myb gene m
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31	14.8	82.2	18	AAQ44436	Antisense oligonuc
32	14.8	82.2	18	AAQ92406	C-myb antisense ol
33	14.8	82.2	18	AAQ88724	Human c-myc modifi
34	14.8	82.2	18	AAQ24194	Phosphononoester
35	14.8	82.2	18	AAQ33910	c-myb expression i
36	14.8	82.2	18	AAQ44240	c-myb antisense co
37	14.8	82.2	18	AAQ28325	Multi-G oligonucle
38	14.8	82.2	18	AAQ17813	Glycosaminoglycan
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40	14.8	82.2	18	AAQ65963	Antisense oligonuc
41	14.8	82.2	18	AAV65963	Antisense oligonuc
42	14.8	82.2	18	AAV28155	Deletion sequence
43	14.8	82.2	18	AAQ23585	Target c-myb antis
44	14.8	82.2	18	AAQ18676	Antisense oligonuc
45	14.8	82.2	18	AAV9427	Human c-myb therap
			18	AAZ98653	

ALIGNMENTS

RESULT 1
AAQ42217
ID AAQ42217 standard; DNA; 18 BP.
XX
AC AAQ42217;
XX
AC AAQ42217;
DT 02-SEP-1993 (first entry)
DE Antisense sequence to mouse c-myb.
XX
KW Antisense; oligonucleotide; inhibit; translation; transcription;
KW target; nucleic acid; mammal; tissue; hybridise; combine; carrier;
KW polyethylene oxide; polypropylene oxide; copolymer; ss.
XX
OS Synthetic.
XX
PN WO9308845-A.
XX
PD 13-MAY-1993.
XX
PF 05-NOV-1992; 92WO-0509626.
XX
PR 08-NOV-1991; 91US-0792146.
PR 18-MAR-1992; 92US-0855416.
(MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
PI Simons M;
XX
DR WPI; 1993-167406/20.
XX

PT Inhibiting translation or transcription of target nucleic acid -
PT by local administration in vivo of oligo:nucleotide complementary
PT to target sequence
XX
XX Disclosure; Page 39; 65pp; English.
XX
CC The sequences given in AAQ42217-21 are antisense oligonucleotides
CC which were used to inhibit translation or transcription of target
CC nucleic acids at a locus in vivo. The oligonucleotide are applied
CC directly to a tissue at the locus within the body of a mammal and
CC they are able to penetrate the cells of the tissue, hybridise/combine
CC with the target nucleic acid inhibiting intracellular translation or
CC transcription. The oligonucleotide are incorporated into a carrier
CC eg. a polyethylene oxide-polypropylene oxide copolymer.
XX
XX Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18
|||||
Db 1 gtgtcgggggtctccgggc 18

RESULT 2
AAQ34766
ID AAQ34766 standard; DNA; 18 BP.
XX
AC AAQ34766;
XX
DT 02-JUN-1993 (first entry)
XX
DE Murine c-myb antisense oligonucleotide.
XX
KW Antisense; inhibit; protein coding genes; regulatory DNA; stroke;
KW endonuclease; vascular restenosis; myocardial infarction; embolism;
KW peripheral muscular disease; peripheral angioplasty; thrombophlebitis;
KW vasculitis; angina; Budd-Chiari syndrome; thrombosis; atherosclerosis;
KW hypertension; primary pulmonary; proliferative glomerulonephritis;
KW acute respiratory distress syndrome; idiopathic pulmonary fibrosis;
KW emphysema; ss.
XX
OS Synthetic.
XX
PN WO9301286-A.
XX
PD 21-JAN-1993.
XX
PF 23-JUN-1992; 92WO-US05305.
XX
PR 28-JUN-1991; 91US-0723454.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI DeKeyser J, Edelman E, Langer RS, Rosenberg RD;
PI Simons M;
XX
XX WPI; 1993-045491/05.
XX
XX Localised therapy using anti-sense oligo:nucleotide(s) - which
XX penetrate through tissue cell to hybridise with target m-RNA and
XX inhibit expression of the gene, for treatment of vascular
XX disorders, atherosclerosis, hypertension, etc.
XX
XX Disclosure; Page 21; 59pp; English.
XX
CC The sequences given in AAQ34766-67 and AAQ35258-60 are antisense
CC oligonucleotides which were used in a method of inhibiting a target
CC nucleic acid sequence. The method may be used for inhibiting the
CC expression of protein coding genes as well as regulatory DNA.

CC Application of the antisense oligonucleotides to a defined locus in
CC vivo allows their use when systemic administration is not possible,
CC ie. systemically administered oligos may be rendered inefficient by
CC endonucleases before they reach their targets. This method may be
CC used in the treatment of vascular disorders, particularly vascular
CC restenosis, myocardial infarction, peripheral muscular disease;
CC peripheral angioplasty, thrombophlebitis, stroke, embolism,
CC vasculitis, angina, Budd-Chiari syndrome, thrombosis, atherosclerosis,
CC hypertension, primary pulmonary hypertension, proliferative glomerulo-
CC nephritis, acute respiratory distress syndrome, idiopathic pulmonary
CC fibrosis or emphysema.
XX
XX Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18
|||||
Db 1 gtgtcgggggtctccgggc 18

RESULT 3
AAQ37635
ID AAQ37635 standard; DNA; 18 BP.
XX
AC AAQ37635;
XX
DT 18-JUN-1993 (first entry)
XX
DE Antisense oligonucleotide to mouse c-myb codons 2-7.
XX
KW Erythrocyte; red blood cell; precursor; haemoglobin; Hb; anaemia;
KW oncogene; haematopoiesis; P75 c-myb; ss.
XX
OS Synthetic.
XX
PN WO9302654-A.
XX
PD 18-FEB-1993.
XX
PF 10-AUG-1992; 92WO-US06685.
XX
PR 09-AUG-1991; 91US-0742867.
XX
PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Sytkowski AJ;
XX
XX WPI; 1993-076139/09.
XX
XX Haemoglobin synthesis inducement in red blood precursor cells -
XX by decreasing levels of differentiation regulator proteins e.g.
XX P75 c-myb regulating transcription of cellular genes for high
XX haemoglobin content
XX
XX Example 4; Page 26; 32pp; English.
XX
XX The product of c-myb is the differentiation regulator protein P75c-
XX myb. Downregulation of this gene, e.g. by antisense oligonucleotides,
XX results in an increase in haemoglobin production in red blood cell
XX precursors. The precursor cells can then be used in the treatment of
XX anaemia or other disorders which result from decreased oxygen-
XX carrying capacity. Oligonucleotide AAQ37635 is an example of an
XX antisense oligonucleotide for inducing Hb synthesis; 17% of cells
XX treated with AAQ37635 were haemoglobinised (Hb+) after 48 hours.
XX Treatment of replicate cultures with antisense c-myb and EPO
XX simultaneously yielded 18% Hb+ cells. The absence of an additive
XX effect suggests that both agents are operating on the same
XX responsive population of cells.

SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
 Db 1 gtgtcgggggtctccgggc 18

RESULT 4
 ID AAT44437 standard; DNA; 18 BP.
 XX
 AC AAT44437;
 DT 27-JAN-1997 (first entry)
 XX
 DE Antisense oligonucleotide against c-myb.
 XX
 KW 8-azapurine; modification; stronger complex; inhibition; ss.
 XX
 OS Synthetic.
 XX
 PN EP680969-A2.
 XX
 PD 08-NOV-1995.
 XX
 PF 26-APR-1995; 95EP-0106230.
 XX
 PR 02-MAY-1994; 94DE-4415370.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Lampe S, Seela F;
 XX
 DR WPI; 1995-375165/49.
 XX
 PT New oligo:nucleotide(s) contg. 8-aza:purine base - useful as
 PT therapeutic and diagnostic agents with more stable hybridisation to
 PT target nucleic acid
 XX
 PS Disclosure; Page 39; 51pp; German.
 XX
 CC AAT44425-54 are antisense oligonucleotides which have at least one
 CC 8-azapurine base. The presence of an 8-azapurine base results in
 CC significantly stronger complexing when hybridising to target nucleic
 CC acids. The present sequence is against c-myb.
 XX
 SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
 Db 1 gtgtcgggggtctccgggc 18

RESULT 5
 ID AAQ88725 standard; DNA; 18 BP.
 XX
 AC AAQ88725;
 XX
 DT 27-FEB-1996 (first entry)
 XX
 DE Mouse c-myc modified antisense oligonucleotide.
 XX

antisense; analogue; non-terminal pyrimidine; phosphorothioate;
 backbone; treatment; HIV; human immunodeficiency virus; HSV;
 herpes simplex virus; cancer; integrin; cell adhesion receptor;
 infection; diagnosis; nuclease resistance; ss.
 XX
 OS Mus musculus.
 XX
 PN EP653439-A2.
 XX
 PD 17-MAY-1995.
 XX
 PF 07-NOV-1994; 94EP-0117513.
 XX
 PR 12-NOV-1993; 93DE-4338704.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Heisberg M, Kretzschmar G, Mag M, Peyman A, Uhlmann E;
 PI Winkler I;
 XX
 DR WPI; 1995-180677/24.
 XX
 PT New anti-sense oligo:nucleotide analogues - with modified
 PT non-terminal pyrimidine nucleotide units, useful for treating viral
 PT infections, cancer, etc.
 XX
 PS Disclosure; Page 25; 36pp; German.
 XX
 CC The antisense oligonucleotide (ON) shown is a derivative of an
 CC equivalent wild type mouse c-myc ON, in which at least one, esp. 2-10,
 CC non-terminal pyrimidine nucleotide(s) is/are modified. The modification
 CC may be: (a) replacement of a phosphodiester linkage by: a
 CC phosphorothioate (PS), -dithioate, -aramidate; borano-, alkyl-,
 CC aralkyl-phosphate; 2,2,2-trichloro-1,1dimethyl-, alkyl- or aryl-,
 CC phosphonate linkage; or (3'-thio)formacetal, methylhydroxylamine, oxime,
 CC methylenedimethylhydrazo, dimethylene sulphone or silyl linkage; (b)
 CC replacement of a sugar phosphate backbone by a 'morpholinonucleoside'
 CC oligomer; (c) replacement of beta-D-2-deoxyribose by another sugar or
 CC carbocyclic, open-chain or bicyclic sugar analogue; or (c) replacement
 CC of the natural nucleoside base by an analogue, e.g.
 CC 5-hydroxymethyl-uridine. The 5' and/or 3' terminus may also be modified
 CC with a lipophilic gp., eg. a farnesyl. The modifications increase
 CC nuclease resistance and thus improve stability and activity.
 XX
 SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
 Db 1 gtgtcgggggtctccgggc 18

RESULT 6
 ID AAT28320 standard; DNA; 18 BP.
 XX
 AC AAT28320;
 XX
 DT 19-NOV-1996 (first entry)
 XX
 DE Multi-G oligonucleotide mu AS (G4).
 XX
 KW Multi-G oligonucleotide; antisense sequence; c-myb; nuclease resistant;
 KW phosphorothioate linkage; phosphorodithioate linkage; inhibitor; therapy;
 KW cell proliferation; smooth muscle cell; proliferation protein;
 KW vascular restenosis; arterial restenosis; ss.
 XX
 OS Synthetic.
 XX

PN	WO9611266-A2.
XX	
PD	18-APR-1996.
XX	
PF	03-OCT-1995; 95WO-US12770.
XX	
PR	05-OCT-1994; 94US-0318458.
XX	
PA	(AMGE-) AMGEN INC.
PI	Burgess TL, Farrell CL, Fisher EF;
DR	WPI; 1996-209848/21.
PT	New modified oligo:nucleotide(s) contg. consecutive guanine residues
PT	- inhibit proliferation of smooth muscle cells, esp. to prevent
PT	arterial restenosis
XX	
XX	Example 1; Page 42; 67pp; English.
PS	
XX	AAT28317-T28347 represent multi-G oligonucleotides. AAT28317-T28324 are
CC	based on an antisense sequence against the c-myc target. These
CC	sequences are oligonucleotides of the invention. These sequences can be
CC	modified to become more nuclease resistant, using phosphorothioate,
CC	phosphordithioate, or 3'-carbon modified links. To screen for modified
CC	multi-G sequences that inhibit cell proliferation, cultured smooth
CC	muscle cells that are arrested in the G0 phase, are induced to
CC	proliferate in the presence of the multi-G sequence. The cultured smooth
CC	muscle cells used in this method are attached to a solid support, and
CC	growth arrest is achieved on a starvation medium, followed by transfer to
CC	a normal growth medium to induce proliferation. The compounds that
CC	provide over 50% inhibition at a set dosage are selected as being useful
CC	for inhibiting vascular restenosis. The multi-G oligonucleotides are
CC	used to inhibit proliferation of smooth muscle cells, such as to prevent
CC	arterial restenosis. These sequences are not antisense sequences, but
CC	are thought to work in a similar way. The sequences are thought to act
CC	by binding to proteins involved in the proliferation process. Compounds
CC	containing these multi-G oligonucleotides are not toxic, and their effect
CC	on cell proliferation is fully reversible.
XX	
SQ	Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;
	Query Match 100.0%; Score 18; DB 17; Length 18;
	Best Local Similarity 100.0%; Pred. No. 30;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 gtatcggggtctccgggc 18
Db	1 gtatcggggtctccgggc 18
RESULT 7	
AAT17811	
ID	AAT17811 standard; DNA; 18 BP.
XX	
AC	AAT17811;
XX	
DT	30-Oct-1996 (first entry)
DE	
XX	Glycosaminoglycan-degrading enzyme inhibitor SIM-AS.
KW	Glycosaminoglycan-degrading enzyme; GDE; inhibitor; endoglycosidase;
KW	heparanase; heparitinase; mammalian; bacterial; platelet; macrophage;
KW	neutrophil; leukocyte; endothelial cell; smooth muscle cell; carcinoma;
KW	tumour cell; activation; proliferation; migration; cancer; inflammation;
KW	autoimmune disorder; infection; pathogenic organism; atherosclerosis;
KW	cardiovascular disease; vascular hyperplasia; restenosis; therapy; ss.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	modified base 1..18


```
FT /*tag= a
FT /note= "phosphorothioate backbone"
PN WO9608559-A1.
XX
XX 21-MAR-1996.
XX
XX 13-SEP-1995; 95WO-AU00600.
XX
XX 14-AUG-1995; 95AU-0004769.
XX 16-SEP-1994; 94AU-0008226.
XX 16-SEP-1994; 94AU-0008227.
XX
XX (CARD-) CARDIAC CRC NOMINEES PTY LTD.
XX
XX Graham L, Underwood PA;
XX WPI; 1996-179936/18.
XX
XX Oligo:nucleotide(s) having sulphur substns. between nucleoside(s) -
PT for inhibiting glycosaminoglycan-degrading enzymes, for treating,
PT e.g. cancer, inflammation, infection or autoimmune disorders.
XX
XX Example 2; Page 33; 73pp; English.
XX
XX AAT17805-T17808, and AAT17810-T17813 represent
CC glycosaminoglycan-degrading enzyme (GDE) inhibitors. The GDEs which
CC these sequences inhibit are endoglycosidases (which cleave
CC glycosaminoglycan chains at internal sites), preferably heparanases (also
CC known as heparitinases) of mammalian or bacterial origin. These
CC sequences can be used for inhibiting GDEs associated with platelets,
CC macrophages, neutrophils, leukocytes, endothelial cells, smooth muscle
CC cells, carcinoma and tumour cells, and bacteria. They can also be used
CC to inhibit smooth muscle cell activation, proliferation or migration.
CC The sequences can be used to treat cancer, inflammation, autoimmune
CC disorders, infection caused by pathogenic organisms, and cardiovascular
CC disease, such as vascular hyperplasia, restenosis and atherosclerosis.
CC These inhibitors can also be used as biochemical reagents for studying
CC GDE activities and mechanisms of enzyme activity.
XX
XX Sequence 18 BP; 4 A; 9 C; 5 G; 0 U; 0 other;
SQ
Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gtgtcgggggtctccgggc 18
Db 18 GTGTCGGGGTCTCCGGGC 1
RESULT 9
AAT93470
ID AAT93470 standard; DNA; 18 BP.
XX
XX AAT93470;
AC
XX 16-FEB-1998 (first entry)
XX
XX C-myb antisense oligonucleotide.
XX
XX c-myb antisense oligonucleotide; biocompatible polymer; plasmid DNA;
KW cell transformation; gene therapy; high density lipoprotein; HDL;
KW low density lipoprotein; LDL; ss.
XX
XX Synthetic.
XX
XX US5679559-A.
PN
XX 21-OCT-1997.
PD
XX 03-JUL-1996; 96US-0675120.
PF
```

```
XX 03-JUL-1996; 96US-0675120.
PR
XX (UTAH ) UNIV UTAH RES FOUND.
PA
XX Akaike T, Kim J, Kim SW, Maruyama A;
PI
XX WPI; 1997-525726/48.
DR
XX Composition for delivering nucleic acid to a cell - comprising
XX complex of nucleic acid with hydrophobised cationic biocompatible
XX polymer and lipoprotein
XX
XX Claim 10; Column 9; 10pp; English.
XX
XX This c-myb antisense oligonucleotide is used in the preparation of a
XX gene delivery composition. The composition comprises a complex of the
XX nucleic acid to be delivered to a cell with a hydrophobised cationic
XX biocompatible polymer and a lipoprotein. One part of the polymer and
XX one part of the lipoprotein can be combined with either one part plasmid
XX DNA or 0.001 to 0.05 parts of this oligonucleotide. The composition is
XX used for transforming cells in vitro.
XX
XX Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gtgtcgggggtctccgggc 18
Db 1 gtgtcgggggtctccgggc 18
RESULT 10
AAAL3831
ID AAAL3831 standard; DNA; 18 BP.
XX
XX AAAL3831;
AC
XX 27-JUL-2000 (first entry)
XX
XX C-myb phosphorothioate antisense oligonucleotide SEQ ID NO:5.
DE
XX Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
XX PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW recurrent stenosis; cardiovascular injury; ss.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..18
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
XX CA2228977-A1.
PN
XX 07-MAY-1999.
PD
XX 03-FEB-1998; 98CA-2228977.
PF
XX 07-NOV-1997; 97CA-2215360.
XX
XX (EDEL/) EDELMAN E R.
XX (ROSE/) ROSENBERG R D.
XX (SIRO/) SIROIS M G.
XX (SINO/) SIMONS M.
XX
XX Edelman ER, Rosenberg RD, Sirosis MG, Simons M;
PI
XX WPI; 2000-283933/25.
DR
XX
```

PT Antisense inhibition of platelet derived growth factor beta-receptor
XX subunit expression for the prevention of restenosis -
PS
PS Claim 27; Page 23; 43pp; English.
XX
CC A method has been developed for preventing restenosis following vascular
CC injury by antisense inhibition of platelet derived growth factor
CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
CC canal), especially of a valve in the heart, after surgical correction of
CC the primary condition) following cardiovascular injury. The present
CC sequence represents a phosphorothioate antisense oligonucleotide for
CC c-myb.
XX
SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
Db 1 gtgtcggggtctccgggc 18

RESULT 11
AAF99482
ID AAF99482 standard; DNA; 18 BP.
XX
AC AAF99482;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #598.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
XX WO200122972-A2.
XX
XX 05-APR-2001.
XX
XX 25-SEP-2000; 2000WO-US26383.
XX
XX 25-SEP-1999; 99US-0156113.
XX
XX 27-SEP-1999; 99US-0156135.
XX
XX 23-AUG-2000; 2000US-0227436.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX
XX (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Schetter C, Vollmer J;
XX
XX WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
XX using immunostimulatory Py-rich and TG nucleic acids -
XX
XX Claim 101; Page 51; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
XX response. The method comprises administering an immunostimulatory nucleic
XX acid to a non-rodent subject in sufficient quantity to stimulate an
XX immune response. The present sequence is one such immunostimulatory
XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,

CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
XX
XX Note: the present sequence may have a phosphorothioate backbone.
XX
SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
Db 1 gtgtcggggtctccgggc 18

RESULT 12
AAF60950
ID AAF60950 standard; DNA; 18 BP.
XX
AC AAF60950;
XX
DT 15-MAY-2001 (first entry)
XX
DE Anti-c-myb oligonucleotide SEQ ID 59.
XX
KW Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
KW antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense;
KW tumor therapy; drug; ss.
XX
OS Unidentified.
XX
XX DE19935302-A1.
XX
XX 08-FEB-2001.
XX
XX 28-JUL-1999; 99DE-1035302.
XX
XX 28-JUL-1999; 99DE-1035302.
XX
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX
XX Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
XX
XX WPI; 2001-203679/21.
XX
XX New substituted aryl conjugates of parent molecules, especially
XX oligonucleotides, having improved transmembrane and intracellular
XX transport properties, useful as medicaments or diagnostic agents -
XX
XX Disclosure; Page 8; 28pp; German.
XX
XX This invention describes a novel conjugate (I) which consists of (A) a
XX molecule to be transported and (B) at least one aryl residue of formula
XX -Ar-(X-C(Y)-R₁)-n (II). Ar = group containing at least one aromatic
XX ring; X = O or N (sic); Y = O, S or NH-R₂ (sic); R₁ = optionally
XX substituted 1-23C alkyl (optionally containing double and/or triple
XX bonds); R₂ = optionally substituted 1-18C alkyl (optionally containing
XX double and/or triple bonds); n = integer of 1 or more. (A) is bonded to
XX (B) directly or via a chemical group, provided that the chemical group is
XX other than CH₂-S if the bond is via a phosphodiester linkage of (A). The
XX invention also describes (i) the preparation of a conjugate (I') of (A')
XX a molecule to be transported and (B') at least one aryl residue (not
XX restricted to (II)), by preparing (A') containing a reactive function at
XX the position at which (B') is to be bonded, preparing (B') and reacting
XX (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded
XX via a chemical group) for transporting (A) across biological membranes.
XX The products of the invention have cytostatic, virucide, vasotropic,
XX dermatological, antipsoriatic and antiasthmatic activity and can be used
XX for gene therapy. Conjugation of (A) with (B) is useful for transporting

CC (A) across biological membranes or into eukaryotic or prokaryotic cells
 CC (specifically bacterial, yeast or mammalian cells, including human cells,
 CC particularly tumor cells). Medicaments, diagnostic agents and test kits
 CC containing (I) are also claimed. Typically (I) are antisense
 CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
 CC treating viral infections or diseases associated with integrins or
 CC cell-cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma);
 CC or labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
 CC hybridization. Conjugation with (B) markedly improves the cellular uptake
 CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
 CC in which case the conjugates (I) are fluorescently labeled, allowing
 CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
 CC is superior to that obtained using other conjugated groups related to
 CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
 CC the scope of (B)) have superior uptake to corresponding fluorescein
 CC conjugates.

XX SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtgtcgggggtctccgggc 18
 |||||
 Db 1 gtgtcgggggtctccgggc 18

RESULT 13
 AAF86998/c

ID AAF86998 standard; DNA; 18 BP.

XX AC AAF86998;

XX DT 13-JUL-2001 (first entry)

XX DE Rat c-myb phosphorothioate sense oligonucleotide.

XX KW Rat; NfkappaB; vitamin E; hepatitis C virus; chronic liver disease;
 XX KW hepatic fibrosis; phosphorothioate backbone; 2,6-di-tert-butylphenol; ss.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT modified_base 1..18

XX FT /*tag= a

XX FT /mod_base= "OTHER"

XX FT /note= "phosphorothioate backbone"

XX PN WO200121166-A1.

XX XX 29-MAR-2001.

XX PF 21-SEP-2000; 2000WO-US25956.

XX PR 21-SEP-1999; 99US-0400322.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chojkier M;

XX DR WPI; 2001-354755/37.

XX XX Treatment of patients suffering from hepatitis C comprises
 PT administration of a 2,6-di-tert-butylphenol derivative -

XX PS Example 2; Page 39; 81pp; English.

XX CC The present invention describes a method of treating hepatitis C virus
 CC infection, involving administering a 2,6-di-tert-butylphenol derivative
 CC to the affected individual. This is particularly useful in patients
 CC refractory to interferon. The present sequence is a sense oligonucleotide

CC with a phosphorothioate backbone, directed at the rat c-myb sequence in a
 CC stellate cell inhibition assay described in the exemplification of the
 CC invention.

XX SQ Sequence 18 BP; 4 A; 9 C; 5 G; 0 U; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtgtcgggggtctccgggc 18
 |||||
 Db 18 GTGTGGGGGTCTCCGGGC 1

RESULT 14

AAF86999
 ID AAF86999 standard; DNA; 18 BP.

XX AC AAF86999;

XX DT 13-JUL-2001 (first entry)

XX DE Rat c-myb phosphorothioate antisense oligonucleotide.

XX KW Rat; NfkappaB; vitamin E; hepatitis C virus; chronic liver disease;
 XX KW hepatic fibrosis; phosphorothioate backbone; 2,6-di-tert-butylphenol; ss.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT modified_base 1..18

XX FT /*tag= a

XX FT /mod_base= "OTHER"

XX FT /note= "phosphorothioate backbone"

XX PN WO200121166-A1.

XX PD 29-MAR-2001.

XX PF 21-SEP-2000; 2000WO-US25956.

XX PR 21-SEP-1999; 99US-0400322.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chojkier M;

XX DR WPI; 2001-354755/37.

XX XX Treatment of patients suffering from hepatitis C comprises
 PT administration of a 2,6-di-tert-butylphenol derivative -

XX PS Example 2; Page 39; 81pp; English.

XX CC The present invention describes a method of treating hepatitis C virus
 CC infection, involving administering a 2,6-di-tert-butylphenol derivative
 CC to the affected individual. This is particularly useful in patients
 CC refractory to interferon. The present sequence is an antisense
 CC oligonucleotide with a phosphorothioate backbone, directed at the rat
 CC c-myb sequence in a stellate cell inhibition assay described in the
 CC exemplification of the invention.

XX SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtgtcgggggtctccgggc 18
 |||||

Db 1 gtgtcggggtctccgggc 18

RESULT 15

AAH49233
ID AAH49233 standard; DNA; 18 BP.

XX AC AAH49233;

DT 26-NOV-2001 (first entry)

XX Anti-c-myb oligonucleotide XXVI.

XX Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.

XX Synthetic.

OS EP1113021-A2.

PN 04-JUL-2001.

PD 08-MAR-1995; 2001EP-0104012.

XX 14-MAR-1994; 94DE-4408528.

PR 08-MAR-1995; 95EP-0103332.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

PA Uhlmann E, Breipohl G;

XX WPI; 2001-591367/67.

XX New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers

XX Disclosure; Page 25; 54pp; German.

XX This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula
CC F((DNA)-Li)-q(PNA)-Li)-r(DNA)-Li)-s(PNA)-t)-xf' where q, r, s, t = 0 or 1,
CC with the sum of two or more adjacent letters at least 2; x = 1-20; DNA
CC = nucleic acid (such as DNA or RNA or their known derivatives); Li =
CC covalent linkage between DNA and PNA, i.e. a bond or a residue containing
CC at least one atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide
CC structure containing at least one nucleobase different from thymine; and
CC F, F' = end groups and/or are connected through a covalent bond. The
CC products of the invention have anticancer, antiproliferative, antiviral,
CC hepatotropic and vasotropic activity and can be used for the inhibition
CC of gene expression by antisense, ribozyme, sense, or triple-helix
CC methods, or by binding to proteins (aptamers). (I) are used for treating
CC diseases caused by viruses (human immune deficiency, herpes simplex,
CC influenza, vesicular stomatitis, hepatitis B or papilloma), or mediated
CC by integrins or cell-cell adhesion reactions, for treating cancer, or
CC for inhibiting restenosis, particularly as antisense reagents. They are
CC also useful in heterogeneous or homogeneous assays as primers or probes,
CC particularly where the target is amplified before being detected by
CC hybridization, for diagnosis of genetic, malignant or pathogen-related
CC diseases. (I) retain the increased affinity for complementary strands and
CC better stability in serum, associated with conventional peptide nucleic
CC acids (PNA), but lack the disadvantages, i.e. have improved cellular
CC uptake, do not aggregate in aqueous solution, and have reduced affinity
CC for purification materials, reduced cytotoxicity, better sequence
CC specificity. They are more active than either DNA or PNA oligomers. When
CC used as probes, (I) show different responses to base-pair mismatches in
CC the DNA and PNA segments, allowing better discrimination between
CC pathogenic and non-pathogenic conditions such as the transition from
CC proto-oncogene to oncogene, also, when used as primers, with the PNA
CC segment at the 5'-end, they produce amplicons resistant to
CC 5'-exonuclease, allowing this enzyme to be used to eliminate RNA or DNA
CC primers. The DNA component allows additional reactions not possible with

CC PNA alone, e.g. 3'-tailing and (I) may be incorporated into a gene.
CC AAH49208-AAH49264 represent oligonucleotides used to illustrate the
CC method of the invention.

XX
SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtgtcggggtctccgggc 18

DB 1 gtgtcggggtctccgggc 18

Search completed: October 12, 2002, 17:08:03

Job time: 9/48 sec

ANTI-SENSE: YES
FEATURE: misc.feature
LOCATION: 1-18
OTHER INFORMATION: /standard_name= "ANTISENSE MOUSE"
OTHER INFORMATION: C-MYB
OTHER INFORMATION: /note= "ANTISENSE SEQUENCE TO MOUSE C-MYB"
US-08-369-282-1

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 2
US-08-445-291-6
; Sequence 6, Application US/08445291
; Patent No. 5649638
; GENERAL INFORMATION:
; APPLICANT: Polushin, Nikolai N.
; APPLICANT: Efimov, Vladimir A.
; APPLICANT: Morocho, Alan M.
; APPLICANT: Cohen, Jack S.
; TITLE OF INVENTION: DEPROTECTION OF OLIGONUCLEOTIDES AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,291
; FILING DATE:
; CLASSIFICATION: 102
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB/J-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-6400
; TELEFAX: (703)836-2787
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-445-291-6

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 3

US-08-445-291-7/c
; Sequence 7, Application US/08445291
; Patent No. 5649638
; GENERAL INFORMATION:
; APPLICANT: Polushin, Nikolai N.
; APPLICANT: Efimov, Vladimir A.
; APPLICANT: Morocho, Alan M.
; APPLICANT: Cohen, Jack S.
; TITLE OF INVENTION: DEPROTECTION OF OLIGONUCLEOTIDES AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,291
; FILING DATE:
; CLASSIFICATION: 102
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB/J-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-6400
; TELEFAX: (703)836-2787
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-445-291-7

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 18 GTGTGGGGGTCTCCGGGC 1

RESULT 4
US-08-675-120-1
; Sequence 1, Application US/08675120
; Patent No. 5679559
; GENERAL INFORMATION:
; APPLICANT: Jin-Seok Kim
; APPLICANT: Atsushi Maruyama
; APPLICANT: Toshihiro Akaie
; APPLICANT: Sung Wan Kim
; TITLE OF INVENTION: CATIONIC POLYMER AND LIPOPROTEIN-
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5679559th & Western, L.L.P.
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

COMPUTER: AST Ascentia 900N
OPERATING SYSTEM: DOS 6.22
SOFTWARE: Word Perfect 6.0
CURRENT APPLICATION DATA: US/08/675,120
FILING DATE: 03-JUL-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Alan J. Howarth
REGISTRATION NUMBER: 36,553
REFERENCE/DOCKET NUMBER: T3622/U-2220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-675-120-1

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 5
US-08-723-052-3/c
; Sequence 3, Application US/08723052
; Patent No. 5922757
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; APPLICANT: Carson, Dennis
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,052
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Christopher J.
; REGISTRATION NUMBER: 40,179
; REFERENCE/DOCKET NUMBER: UCSD-02424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/705-8410
; TELEFAX: 415/397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-723-052-3

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 18 GTGTGGGGGTCTCCGGGC 1

RESULT 6
US-08-723-052-4
; Sequence 4, Application US/08723052
; Patent No. 5922757
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; APPLICANT: Carson, Dennis
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,052
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Christopher J.
; REGISTRATION NUMBER: 40,179
; REFERENCE/DOCKET NUMBER: UCSD-02424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/705-8410
; TELEFAX: 415/397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-723-052-4

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
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Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 7
US-08-578-686C-25
; Sequence 25, Application US/08578686C
; Patent No. 6028182
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; TITLE OF INVENTION: Methylphosphonic Acid Ester, Process For
; PREPARING THE SAME AND ITS USE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.

```
; STREET: 1300 I. Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,686C
; FILING DATE: January 2, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 2481.1481-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-578-686C-25

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
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Db 1 GTGTGGGGTCTCCGGGC 18

RESULT 8
US-09-944-405-13
; Sequence 13, Application US/09094405
; Patent No. 6066720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified oligonucleotides, their preparation
; TITLE OF INVENTION: and use
; NUMBER OF SEQUENCES: 30
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,405
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,196
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Mous
; FEATURE:
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; NAME/KEY: exon
; LOCATION: 1..18
; OTHER INFORMATION: /note= "c-myb"
; US-09-094-405-13

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
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Db 1 GTGTGGGGTCTCCGGGC 18

RESULT 9
US-09-274-625-3/c
; Sequence 3, Application US/09274625
; Patent No. 6075027
; GENERAL INFORMATION:
; APPLICANT: Choikier, Mario
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HEPATIC DISORDERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/274,625
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/274,624
; FILING DATE: 23-MAR-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UCSD-03683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/705-8410
; TELEFAX: 415/397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-274-625-3

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
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Db 18 GTGTGGGGTCTCCGGGC 1

RESULT 10
US-09-274-625-4
; Sequence 4, Application US/09274625
; Patent No. 6075027
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```

1  RESULT 11
2  US-09-274-624-3/c
3  ; Sequence 3, Application US/09274624
4  ; Patent No. 6147123
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Chojkier, Mario
7  ; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
8  ; TITLE OF INVENTION: HEPATIC DISORDERS
9  ; NUMBER OF SEQUENCES: 4
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: MEDDEN & CARROLL, LLP
12 ; STREET: 220 Montgomery Street, Suite 2200
13 ; CITY: San Francisco
14 ; STATE: California
15 ; COUNTRY: United States of America
16 ; ZIP: 94104
17 ;
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC Compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/09/274,624
25 ;

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/274,624
FILING DATE: 23-MAR-1999
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UCSD-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-274-624-4

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Query Match      100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. NO. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels
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QY 1 gtgtcggggtctccgggc 18
|||||
Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 13
US-09-144-112-25
; Sequence 25, Application US/09144112
; Patent No. 6150510
; GENERAL INFORMATION:
; APPLICANT: SEELA, Frank
; APPLICANT: THOMAS, Horst
; TITLE OF INVENTION: MODIFIED OLIGONUCLEOTIDES, THEIR PREPARATION AND THEIR
; FILE REFERENCE: 026083/0181
; CURRENT APPLICATION NUMBER: US/09/144,112
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: DE P 44 38 918.3
; PRIOR FILING DATE: 1994-11-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antisense
; OTHER INFORMATION: Oligonucleotide
US-09-144-112-25

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
QY 1 gtgtcggggtctccgggc 18
|||||
Db 1 gtgtcggggtctccgggc 18

RESULT 14
US-09-400-322-3/c
; Sequence 3, Application US/09400322
; Patent No. 6218437
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS
; FILE REFERENCE: UCSD-03831
; CURRENT APPLICATION NUMBER: US/09/400,322
; CURRENT FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: 08/723,052
; EARLIER FILING DATE: 1996-09-30
; EARLIER APPLICATION NUMBER: 09/274,624
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: 09/274,625
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-400-322-3

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
QY 1 gtgtcggggtctccgggc 18

Db 18 GTGTCGGGGTCTCCGGGC 1
|||||
RESULT 15
US-09-400-322-4
; Sequence 4, Application US/09400322
; Patent No. 6218437
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS
; FILE REFERENCE: UCSD-03831
; CURRENT APPLICATION NUMBER: US/09/400,322
; CURRENT FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: 08/723,052
; EARLIER FILING DATE: 1996-09-30
; EARLIER APPLICATION NUMBER: 09/274,624
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: 09/274,625
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-400-322-4

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
QY 1 gtgtcggggtctccgggc 18
|||||
Db 1 gtgtcggggtctccgggc 18

Search completed: October 12, 2002, 16:54:37
Job time: 8992 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:31 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-5

Perfect score: 18

Sequence: 1 gtgtcgggggtctccggcg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 4: /cgn2_6/ptodata/2/pna/US080_COMB.seq.*
 - 5: /cgn2_6/ptodata/2/pna/US081_COMB.seq.*
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- 63: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
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- 66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
- 67: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*
- 68: /cgn2_6/ptodata/2/pna/US6029_COMB.seq.*
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- 70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
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- 72: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
- 73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	1	PCT-US97-12425-1
2	18	100.0	18	3	US-07-742-867-1
3	18	100.0	18	3	US-07-928-114-1
4	18	100.0	18	3	US-07-928-114A-1
5	18	100.0	18	5	US-08-145-701-6
6	18	100.0	18	5	US-08-145-701-7
7	18	100.0	18	7	US-08-318-458A-4
8	18	100.0	18	8	US-08-402-838-25
9	18	100.0	18	8	US-08-480-216-4
10	18	100.0	18	8	US-08-486-490-4
11	18	100.0	18	13	US-08-940-196-13
12	18	100.0	18	16	US-09-241-561-5
13	18	100.0	18	24	US-09-627-787-59
14	18	100.0	18	25	US-09-643-233-25
15	18	100.0	18	26	US-09-669-187A-661
16	18	100.0	18	29	US-09-724-600-3
17	18	100.0	18	29	US-09-724-600-4
18	18	100.0	18	29	US-09-724-664-3
19	18	100.0	18	29	US-09-724-664-4
20	18	100.0	18	29	US-09-724-667-3
21	18	100.0	18	29	US-09-724-667-4
22	18	100.0	18	29	US-09-724-694-3
23	18	100.0	18	29	US-09-724-694-4
24	18	100.0	18	29	US-09-724-695-3
25	18	100.0	18	29	US-09-724-695-4
26	18	100.0	18	29	US-09-724-870-3
27	18	100.0	18	29	US-09-724-870-4
28	18	100.0	18	30	US-09-793-146-25
29	18	100.0	18	32	US-09-835-370-48
30	18	100.0	18	32	US-09-835-371-48
31	18	100.0	18	33	US-09-888-326-474

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32      18 100.0      18 37 US-10-017-995-661      Sequence 661, App
33      16.4 91.1      18 7 US-08-318-458A-1      Sequence 1, Appli
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36      16.4 91.1      18 7 US-08-318-458A-7      Sequence 7, Appli
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38      16.4 91.1      18 8 US-08-480-216-3      Sequence 3, Appli
39      16.4 91.1      18 8 US-08-480-216-7      Sequence 7, Appli
40      16.4 91.1      18 8 US-08-486-490-1      Sequence 1, Appli
41      16.4 91.1      18 8 US-08-486-490-3      Sequence 3, Appli
42      16.4 91.1      18 8 US-08-486-490-7      Sequence 7, Appli
43      16.4 91.1      18 26 US-09-669-187A-628      Sequence 628, App
44      16.4 91.1      18 26 US-09-669-187A-662      Sequence 662, App
45      16.4 91.1      18 33 US-09-888-326-468      Sequence 468, App
46      16.4 91.1      18 33 US-09-888-326-469      Sequence 469, App

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ALIGNMENTS

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RESULT 1
PCT-US97-12425-1
; Sequence 1, Application PC/TUS9712425
; GENERAL INFORMATION:
; APPLICANT: Jin-Seok Kim
; APPLICANT: Atsushi Maruyama
; APPLICANT: Toshihiro Akaiki
; APPLICANT: Sung Wan Kim
; TITLE OF INVENTION: CATIONIC POLYMER AND LIPOPROTEIN-
; TITLE OF INVENTION: CONTAINING SYSTEM FOR GENE DELIVERY
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, North & Western, L.L.P.
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: AST Ascentia 900N
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: Word Perfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12425
; FILING DATE: 03-JUL-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan J. Howarth
; REGISTRATION NUMBER: 36,553
; REFERENCE/DOCKET NUMBER: T3622/U-2220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801)566-6633
; TELEFAX: (801)566-0750
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US97-12425-1

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Query Match      100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTCGGGGTCTCGGCGC 18

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RESULT 2
US-07-742-867-1

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; Sequence 1, Application US/07742867
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; TITLE OF INVENTION: A Method Of Producing Red Blood Cells
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/742,867
; FILING DATE: 19910809
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: NEDH91-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-742-867-1

Query Match      100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTCGGGGTCTCGGCGC 18

RESULT 3
US-07-928-114-1
; Sequence 1, Application US/07928114
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; TITLE OF INVENTION: A METHOD OF INDUCING HEMOGLOBIN
; TITLE OF INVENTION: SYNTHESIS IN RED BLOOD CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02713
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,114
; FILING DATE: 19920810
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,867

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;; FILING DATE: 09-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: NEDH91-05A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-861-6240
;; TELEFAX: 617-861-9540
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-07-928-114-1

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 4
US-07-928-114A-1
;; Sequence 1, Application US/07928114A
;; GENERAL INFORMATION:
;; APPLICANT: Sytkowski, Arthur J.
;; TITLE OF INVENTION: A METHOD OF INDUCING HEMOGLOBIN
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02713

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,114A

FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,867
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: NEDH91-05A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-928-114A-1

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTCGGGGTCTCCGGGC 18
RESULT 5
US-08-145-701-6
;; Sequence 6, Application US/08145701
;; GENERAL INFORMATION:
;; APPLICANT: Polushin, Nikolai N.
;; APPLICANT: Efimov, Vladimir A.
;; APPLICANT: Morochko, Alan M.
;; APPLICANT: Cohen, Jack S.
;; TITLE OF INVENTION: DEPROTECTION OF OLIGONUCLEOTIDES AND
;; ANALOGS
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oliff & Berridge
;; STREET: P.O. Box 19928
;; CITY: Alexandria
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,701
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB/J-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-6400
TELEFAX: (703)836-2787
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-145-701-6

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcggggtctccgggc 18
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Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 6
US-08-145-701-7/c
;; Sequence 7, Application US/08145701
;; GENERAL INFORMATION:
;; APPLICANT: Polushin, Nikolai N.
;; APPLICANT: Efimov, Vladimir A.
;; APPLICANT: Morochko, Alan M.
;; APPLICANT: Cohen, Jack S.
;; TITLE OF INVENTION: DEPROTECTION OF OLIGONUCLEOTIDES AND
;; ANALOGS
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oliff & Berridge
;; STREET: P.O. Box 19928
;; CITY: Alexandria
;; STATE: VA

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; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,701
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB/J-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-6400
; TELEFAX: (703)836-2787
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-145-701-7

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 gtgtcgggggtctccgggc 18
Db 18 GTGTCGGGGTCTCCGGGC 1
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RESULT 7
US-08-318-458A-4
; Sequence 4, Application US/08318458A
; GENERAL INFORMATION:
; APPLICANT: Burgess, Teresa L.
; APPLICANT: Farrell, Catherine L.
; TITLE OF INVENTION: Method for Inhibiting
; TITLE OF INVENTION: Smooth Muscle Cell
; TITLE OF INVENTION: Proliferation and
; TITLE OF INVENTION: Oligonucleotides for
; TITLE OF INVENTION: Use Therein
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Dr.
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh OS 7.0
; SOFTWARE: Microsoft Word Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,458A
; FILING DATE: 05OCT1994
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
;
US-08-318-458A-4
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Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 gtgtcgggggtctccgggc 18
Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 8
US-08-402-838-25
; Sequence 25, Application US/08402838
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Breipohl, Gerhard
; TITLE OF INVENTION: Polymide-Oligonucleotide Derivatives,
; TITLE OF INVENTION: Their Preparation And Use
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Hendersonn Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,838
; FILING DATE: 13-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Warnement, Thalia V.
; REGISTRATION NUMBER: 39,064
; REFERENCE/DOCKET NUMBER: 02481.1437-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-402-838-25
```

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Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 gtgtcgggggtctccgggc 18
Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 9
US-08-480-216-4
; Sequence 4, Application US/08480216
; GENERAL INFORMATION:
; APPLICANT: Burgess, Teresa L.
; APPLICANT: Farrell, Catherine L.
; APPLICANT: Fisher, Eric F.
; TITLE OF INVENTION: Method for Inhibiting
; TITLE OF INVENTION: Smooth Muscle Cell
; TITLE OF INVENTION: Proliferation and
;
US-08-480-216-4
```

;; TITLE OF INVENTION: Oligonucleotides for
;; TITLE OF INVENTION: Use Therein
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: 1840 Dehavilland Dr.
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: USA
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh OS 7.0
;; SOFTWARE: Microsoft Word Version 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/480,216
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/318,458
;; FILING DATE: 05-OCT-1994
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; US-08-480-216-4

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTCTGGGGTCTCCGGGC 18

RESULT 10
US-08-486-490-4
;; Sequence 4, Application US/08486490
;; GENERAL INFORMATION:
;; APPLICANT: Burgess, Teresa L.
;; APPLICANT: Farrell, Catherine L.
;; APPLICANT: Fisher, Eric F.
;; TITLE OF INVENTION: Method for Inhibiting
;; TITLE OF INVENTION: Smooth Muscle Cell
;; TITLE OF INVENTION: Proliferation and
;; TITLE OF INVENTION: Oligonucleotides for
;; TITLE OF INVENTION: Use Therein
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: 1840 Dehavilland Dr.
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: USA
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh OS 7.0
;; SOFTWARE: Microsoft Word Version 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,490
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/318,458
;; FILING DATE: 05-OCT-1994

;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; US-08-486-490-4

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTCTGGGGTCTCCGGGC 18

RESULT 11
US-08-940-196-13
;; Sequence 13, Application US/08940196
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Modified oligonucleotides, their preparation
;; TITLE OF INVENTION: and use
;; NUMBER OF SEQUENCES: 30
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA: US/08/940,196
;; FILING DATE:
;; CLASSIFICATION: 536
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Mous
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 1..18
;; OTHER INFORMATION: /note= "c-myb"
;; US-08-940-196-13

Query Match 100.0%; Score 18; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTCTGGGGTCTCCGGGC 18

RESULT 12
US-09-241-561-5
;; Sequence 5, Application US/09241561
;; GENERAL INFORMATION:
;; APPLICANT: SIROIS, Martin G.
;; APPLICANT: EDELMAN, Elazer R.
;; APPLICANT: ROSENBERG, Robert D.
;; APPLICANT: SIMONS, Michael
;; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
;; TITLE OF INVENTION: Restenosis

```
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-5
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```
Query Match          100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gtgtcggggtctccgggc 18
   |||||
Db 1 gtgtcggggtctccgggc 18
```

```
RESULT 13
US-09-627-787-59
; Sequence 59, Application US/09627787
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Greiner, Beate
; APPLICANT: Unger, Eberhard
; APPLICANT: Gothe, Gislinde
; APPLICANT: Schwerdel, Marc
; TITLE OF INVENTION: CONJUGATES AND PROCESSES FOR THEIR PREPARATION AND
; TITLE OF INVENTION: THEIR USE FOR TRANSPORTING MOLECULES ACROSS BIOLOGICAL
; TITLE OF INVENTION: MEMBRANES
; FILE REFERENCE: 02481.1679
; CURRENT APPLICATION NUMBER: US/09/627,787
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: DE 19935302.6
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-627-787-59
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```
Query Match          100.0%; Score 18; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 gtgtcggggtctccgggc 18
   |||||
Db 1 gtgtcggggtctccgggc 18
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RESULT 14
US-09-643-233-25
; Sequence 25, Application US/09643233
; GENERAL INFORMATION:
; APPLICANT: SEELA, Frank
; APPLICANT: THOMAS, Horst
; TITLE OF INVENTION: MODIFIED OLIGONUCLEOTIDES, THEIR PREPARATION AND THEIR
; TITLE OF INVENTION: USE
```

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; FILE REFERENCE: 026083/0181
; CURRENT APPLICATION NUMBER: US/09/643,233
; CURRENT FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/144,112
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antisense
; OTHER INFORMATION: Oligonucleotide
US-09-643-233-25
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```
Query Match          100.0%; Score 18; DB 25; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 gtgtcggggtctccgggc 18
   |||||
Db 1 gtgtcggggtctccgggc 18
```

```
RESULT 15
US-09-669-187A-661
; Sequence 661, Application US/09669187A
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/669,187A
; CURRENT FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 661
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-669-187A-661
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```
Query Match          100.0%; Score 18; DB 26; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 gtgtcggggtctccgggc 18
   |||||
Db 1 gtgtcggggtctccgggc 18
```

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Search completed: October 12, 2002, 20:42:31
Job time: 16401 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:30 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-5
Perfect score: 18
Sequence: 1 gtgtcgggggtctccgggc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 169489300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Pending_Patents_NA_New.*
- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
 - 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
 - 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
 - 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
 - 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
 - 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
 - 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
 - 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-5
2	18	100.0	18	5	US-09-945-166A-6
3	18	100.0	18	5	US-09-945-166A-7
4	18	100.0	18	5	US-09-776-479-661
5	18	100.0	18	7	US-10-112-653-634
6	16.4	91.1	18	5	US-09-776-479-628
7	16.4	91.1	18	5	US-09-776-479-628
8	16.4	91.1	18	7	US-10-112-653-604
9	16.4	91.1	18	7	US-10-112-653-635
10	14.8	82.2	18	5	US-09-315-298C-9
11	13.8	76.7	30	1	PCT-US02-05625-34
12	13.4	74.4	50	5	US-09-718-321A-1058
13	12.6	70.0	15	1	PCT-US02-14004-18
14	12.4	68.9	25	5	US-09-396-196G-24964
15	12.4	68.9	25	6	US-10-215-112-2404
16	12.2	67.8	24	5	US-09-852-416-18
17	12.2	67.8	25	5	US-09-396-196G-61672
18	12.2	67.8	40	1	PCT-US02-25940-9670
19	12	66.7	13	5	US-09-509-152C-1893
20	12	66.7	14	5	US-09-509-152C-1894
21	12	66.7	15	5	US-09-509-152C-1442
22	12	66.7	18	5	US-09-509-152C-1368
23	11.8	65.6	25	5	US-09-956-604-104106
24	11.8	65.6	25	5	US-09-956-604-123889
25	11.8	65.6	25	5	US-09-396-196G-114792

c	26	11.8	65.6	44	1	PCT-US01-47994-11	Sequence 11, Appl
c	27	11.8	65.6	44	1	PCT-US01-47994-12	Sequence 12, Appl
c	28	11.6	64.4	20	1	PCT-US02-25940-14621	Sequence 14621, A
c	29	11.6	64.4	20	1	PCT-US02-25940-14622	Sequence 14622, A
c	30	11.6	64.4	20	5	US-09-858-152A-6	Sequence 6, Appl
c	31	11.6	64.4	25	5	US-09-396-196G-35792	Sequence 35792, A
c	32	11.6	64.4	25	5	US-09-396-196G-35793	Sequence 35793, A
c	33	11.6	64.4	29	7	US-10-913-970-12	Sequence 12, Appl
c	34	11.6	64.4	38	5	US-09-745-237A-2930	Sequence 2930, Ap
c	35	11.6	64.4	38	5	US-09-745-237A-2940	Sequence 2940, Ap
c	36	11.6	64.4	38	5	US-09-745-237A-3074	Sequence 3074, Ap
c	37	11.6	64.4	38	5	US-09-745-237A-3086	Sequence 3086, Ap
c	38	11.6	64.4	38	5	US-09-745-237A-3099	Sequence 3099, Ap
c	39	11.6	64.4	38	5	US-09-745-237A-3102	Sequence 3102, Ap
c	40	11.6	64.4	40	6	US-10-208-304-9	Sequence 9, Appl
c	41	11.6	64.4	41	1	PCT-US02-25943-31780	Sequence 31780, A
c	42	11.6	64.4	47	7	US-10-170-097-1163	Sequence 1163, Ap
c	43	11.4	63.3	15	1	PCT-US02-25940-1165	Sequence 1165, Ap
c	44	11.4	63.3	15	1	PCT-US02-25940-15037	Sequence 15037, A
c	45	11.4	63.3	17	7	US-10-156-306-5937	Sequence 5937, Ap

ALIGNMENTS

RESULT 1
US-09-945-131-5
; Sequence 5, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazar R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-5

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
Db 1 gtgtcgggggtctccgggc 18

RESULT 2
US-09-945-166A-6
; Sequence 6, Application US/09945166A
; GENERAL INFORMATION:
; APPLICANT: ELMALAH, DAVID R.
; APPLICANT: FISCHMAN, ALAN J.
; APPLICANT: BABICH, JOHN W.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID CONSTRUCTS AND USES RELATED
; TITLE OF INVENTION: THERETO

```
; FILE REFERENCE: MGA-003.01
; CURRENT APPLICATION NUMBER: US/09/945,166A
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-945-166A-6
```

```
Query Match          100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gtgtcggggtctccgggc 18
   |||||
Db 1 gtgtcggggtctccgggc 18
```

RESULT 3

```
US-09-945-166A-7/c
; Sequence 7, Application US/09945166A
; GENERAL INFORMATION:
; APPLICANT: ELMALEH, DAVID R.
; APPLICANT: FISCHMAN, ALAN J.
; APPLICANT: BABICH, JOHN W.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID CONSTRUCTS AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: MGA-003.01
; CURRENT APPLICATION NUMBER: US/09/945,166A
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-945-166A-7
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```
Query Match          100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 gtgtcggggtctccgggc 18
   |||||
Db 18 GTGTGGGGGTCTCCGGGC 1
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RESULT 4

```
US-09-776-479-661
; Sequence 661, Application US/09776479
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/NAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 661
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-661
```

```
Query Match          100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gtgtcggggtctccgggc 18
   |||||
Db 1 gtgtcggggtctccgggc 18
```

RESULT 5

```
US-10-112-653-634
; Sequence 634, Application US/10112653
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 634
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-634
```

```
Query Match          100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 gtgtcggggtctccgggc 18
   |||||
Db 1 gtgtcggggtctccgggc 18
```

RESULT 6

```
US-09-776-479-628
; Sequence 628, Application US/09776479
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/NAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 628
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
```


US-09-776-479-628

Query Match 91.1%; Score 16.4; DB 5; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gtgtcggggtctccggc 18
||| ||||| |||||
Db 1 gtgccggggtctccggc 18

RESULT 7

US-10-112-653-662
; Sequence 662, Application US/09776479
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 662
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-662

Query Match 91.1%; Score 16.4; DB 5; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gtgtcggggtctccggc 18
||| ||||| |||||
Db 1 gtgccggggtctccggc 18

RESULT 8

US-10-112-653-604
; Sequence 604, Application US/10112653
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 604
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-604

Query Match 91.1%; Score 16.4; DB 7; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-112-653-635

Qy 1 gtgtcggggtctccggc 18
||| ||||| |||||
Db 1 gtgccggggtctccggc 18
RESULT 9
US-10-112-653-635
; Sequence 635, Application US/10112653
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 635
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-635

Query Match 91.1%; Score 16.4; DB 7; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gtgtcggggtctccggc 18
||| ||||| |||||
Db 1 gtgccggggtctccggc 18

RESULT 10

US-09-315-298C-9
; Sequence 9, Application US/09315298C
; GENERAL INFORMATION:
; APPLICANT: Teng, Ching-Leou
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Tillman, Lloyd
; APPLICANT: Hardee, Gregory E.
; APPLICANT: Ecker, David J.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Compositions And Methods For Non-Parental Delivery of Oligonuc
; FILE REFERENCE: ISIS3510
; CURRENT APPLICATION NUMBER: US/09/315,298C
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 08/082,624
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Sequence
US-09-315-298C-9

Query Match 82.2%; Score 14.8; DB 5; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtgtcggggtctccggc 18
||| ||||| |||||
Db 1 gtgccggggtctccggc 18

RESULT 11
PCT-US02-05625-34/c
; Sequence 34, Application PC/TUS0205625
; GENERAL INFORMATION:
; APPLICANT: Arena Pharmaceuticals, Inc.
; TITLE OF INVENTION: Endogenous And Non-Endogenous, Constitutively Activated G Protein
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0321
; CURRENT APPLICATION NUMBER: PCT/US02/05625
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Novel Sequence
PCT-US02-05625-34

Query Match 76.7%; Score 13.8; DB 1; Length 30;
Best Local Similarity 88.2%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtctcgggggtctccggg 17
||| ||||| |||||
Db 23 GTCTCGGGGCTCCGGG 7

RESULT 12
US-09-718-321A-1058/c
; Sequence 1058, Application US/09718321A
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/09/718,321A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/163,783
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 1058
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; FEATURE:
; OTHER INFORMATION: single nucleotide polymorphism
; NAME/KEY: misc feature
; LOCATION: (25)...(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43135797
US-09-718-321A-1058

Query Match 74.4%; Score 13.4; DB 5; Length 50;
Best Local Similarity 93.3%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gtctcgggggtctccggg 17
||| ||||| |||||
Db 26 GTCCGGGTCCTCCGGG 12

RESULT 13
PCT-US02-14004-18
; Sequence 18, Application PC/TUS0214004
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshy, Beena
; APPLICANT: Rounds, Eileen
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE RXRB GENE
; FILE REFERENCE: MMH-0480PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14004
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/287,960
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14004-18

Query Match 70.0%; Score 12.6; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2e+04; 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 tgtcgggggtctcc 14
|||||:||||
Db 1 tgtcgggkctcc 13

RESULT 14
US-09-396-196G-24964/c
; Sequence 24964, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Afymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24964
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24964

Query Match 68.9%; Score 12.4; DB 5; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 cggggtctccgggc 18
||||| |||||
Db 14 CGGGGTCTCTCTGC 1

RESULT 15
US-10-215-112-2404/c
; Sequence 2404, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:

; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2404
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2404

Query Match 68.9%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gtcggggtctccgg 16
||||| |||||
Db 14 GTCGGGGCTCCGG 1

Search completed: October 12, 2002, 17:27:31
Job time: 10806 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:03 ; Search time 792.17 seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-6

Perfect score: 18

Sequence: 1 catgtctccacattgga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
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19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	14	AAQ42218
2	18	100.0	18	14	AAQ42218
3	18	100.0	18	21	AAQ34767
4	14.8	82.2	30	18	AAQ13832
5	14.8	82.2	30	18	AAQ43352
6	14.8	82.2	34	18	AAQ43356
7	14.8	82.2	36	21	AAQ43354
8	13.8	76.7	41	18	AAQ35676
9	13.8	76.7	41	19	AAQ18847

c 10	13.8	76.7	41	20	AAQ78449
c 11	13.4	74.4	23	22	AAQ69745
c 12	13.2	73.3	20	21	AAQ34849
c 13	13.2	73.3	20	21	AAQ34797
c 14	13.2	73.3	24	22	AAQ19003
c 15	13.2	73.3	24	22	AAQ19025
c 16	13.2	73.3	28	22	AAQ80037
c 17	13.2	73.3	30	20	AAQ19510
c 18	13.2	73.3	36	22	AAQ31157
c 19	13.2	73.3	36	22	AAQ31158
c 20	13.2	73.3	50	21	AAQ53009
c 21	13.2	73.3	50	21	AAQ53010
c 22	12.8	71.1	22	21	AAQ88926
c 23	12.8	71.1	23	20	AAQ09332
c 24	12.8	71.1	24	20	AAQ09347
c 25	12.8	71.1	25	21	AAQ10590
c 26	12.8	71.1	29	21	AAQ76231
c 27	12.8	71.1	33	19	AAQ71008
c 28	12.8	71.1	33	21	AAQ00051
c 29	12.8	71.1	35	17	AAQ36519
c 30	12.8	71.1	37	15	AAQ69217
c 31	12.8	71.1	45	21	AAQ58499
c 32	12.8	71.1	45	21	AAQ37213
c 33	12.8	71.1	45	22	AAQ54319
c 34	12.8	71.1	48	23	AAQ09114
c 35	12.8	71.1	49	19	AAQ30374
c 36	12.4	68.9	18	21	AAQ53246
c 37	12.4	68.9	20	20	AAQ05992
c 38	12.4	68.9	23	20	AAQ24437
c 39	12.4	68.9	27	21	AAQ36366
c 40	12.4	68.9	29	21	AAQ88022
c 41	12.4	68.9	45	16	AAQ94195
c 42	12.4	68.9	45	16	AAQ94196
c 43	12.4	68.9	45	21	AAQ53225
c 44	12.4	68.9	45	21	AAQ88934
c 45	12.4	68.9	50	11	AAQ06701

ALIGNMENTS

RESULT	1
AAQ42218	
ID	AAQ42218 standard; DNA; 18 BP.
XX	
AC	AAQ42218;
XX	
DT	02-SEP-1993 (first entry)
XX	
DE	Antisense sequence to human NMHC.
XX	
KW	Antisense; oligonucleotide; inhibit; translation; transcription;
KW	target; nucleic acid; mammal; tissue; hybridise; combine; carrier;
KW	polyethylene oxide; polypropylene oxide; copolymer; ss.
XX	
OS	Synthetic.
XX	
PN	WO9308845-A.
XX	
PD	13-MAY-1993.
XX	
PF	05-NOV-1992; 92WO-US09626.
XX	
PR	08-NOV-1991; 91US-0792146.
PR	18-MAR-1992; 92US-0855416.
XX	
PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.
XX	
PI	Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
PI	Simons M;
XX	
DR	WPI; 1993-167406/20.
XX	

HIV gag gene (OSRN
Human IL4Alpha ge
Feline CTLA-4 3' p
Cat CTLA-4 recepto
Reverse primer use
Reverse primer use
PCR primer used to
Human lipocalin ho
Mutagenic primer #
Mutagenic primer #
Aspergillus niger
Aspergillus niger
Hepatitis B virus
Synthetic liposam
Pseudomonas sp. st
Probe specific for
E. coli Argu trNA
PCR primer Smad2-t
Smad2-top PCR prim
Primer to amplify
PCR primer C363CC
Human PRO1283 (UNQ
Human PRO1283 hydr
Probe #26 used in
Human CD20 Amberzy
Oligomer p49rg12 u
P450 polymorphism
PCR primer used to
CAT CTLA4 downstre
PCR primer Guava-u
Human neuroblastom
Transmembrane olig
Transmembrane olig
Human G-protein co
Hepatitis B virus
:HBV.LLA2C.56 ampl

PT Inhibiting translation or transcription of target nucleic acid -
PT by local administration in vivo of oligo:nucleotide complementary
PT to target sequence
XX
PS Disclosure; Page 40; 65pp; English.
XX
CC The sequences given in AAQ42217-21 are antisense oligonucleotides
CC which were used to inhibit translation or transcription of target
CC nucleic acids at a locus in vivo. The oligonucleotide are applied
CC directly to a tissue at the locus within the body of a mammal and
CC they are able to penetrate the cells of the tissue, hybridise/combine
CC with the target nucleic acid inhibiting intracellular translation or
CC transcription. The oligonucleotide are incorporated into a carrier
CC eg. a polyethylene oxide-polypropylene oxide copolymer.
XX
SQ Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccacacttggga 18
DB 1 catgtctccacacttggga 18

RESULT 2
AAQ34767
ID AAQ34767 standard; DNA; 18 BP.
XX
AC AAQ34767;
XX
DT 02-JUN-1993 (first entry)
XX
DE Nonmuscle myosin (NMHC) antisense oligonucleotide.
XX
KW Antisense; inhibit; protein coding genes; regulatory DNA; stroke;
KW endonuclease; vascular restenosis; myocardial infarction; embolism;
KW peripheral muscular disease; peripheral angioplasty; thrombophlebitis;
KW vasculitis; angina; Budd-Chiari syndrome; thrombosis; atherosclerosis;
KW hypertension; primary pulmonary; proliferative glomerulonephritis;
KW acute respiratory distress syndrome; idiopathic pulmonary fibrosis;
KW emphysema; ss.
XX
OS Synthetic.
XX
PN WO9301286-A.
XX
PD 21-JAN-1993.
XX
PF 23-JUN-1992; 92WO-0505305.
XX
PR 28-JUN-1991; 91US-0723454.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
PI Simons M;
XX
WPI; 1993-045491/05.
XX
XX Localised therapy using anti-sense oligo:nucleotide(s) - which
XX penetrate through tissue cell to hybridise with target m-RNA and
PT inhibit expression of the gene, for treatment of vascular
PT disorders, atherosclerosis, hypertension, etc.
XX
PS Disclosure; Page 21; 59pp; English.
XX
CC The sequences given in AAQ34766-67 and AAQ35258-60 are antisense
CC oligonucleotides which were used in a method of inhibiting a target
CC nucleic acid sequence. The method may be used for inhibiting the
CC expression of protein coding genes as well as regulatory DNA.

CC Application of the antisense oligonucleotides to a defined locus in
CC vivo allows their use when systemic administration is not possible,
CC ie. systemically administered oligos may be rendered inefficient by
CC endonucleases before they reach their targets. This method may be
CC used in the treatment of vascular disorders, particularly vascular
CC restenosis, myocardial infarction, peripheral muscular disease;
CC peripheral angioplasty, thrombophlebitis, stroke, embolism,
CC vasculitis, angina, Budd-Chiari syndrome, thrombosis, atherosclerosis,
CC hypertension, primary pulmonary hypertension, proliferative glomerulo-
CC nephritis, acute respiratory distress syndrome, idiopathic pulmonary
CC fibrosis or emphysema.
XX
SQ Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccacacttggga 18
DB 1 catgtctccacacttggga 18

RESULT 3
AA13832
ID AA13832 standard; DNA; 18 BP.
XX
AC AA13832;
XX
DT 27-JUL-2000 (first entry)
XX
DE NMHC phosphorothioate antisense oligonucleotide SEQ ID NO:6.
XX
KW Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW recurrent stenosis; cardiovascular injury; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FH modified_base 1..18
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
CA2228977-A1.
XX
XX 07-MAY-1999.
XX
XX 03-FEB-1998; 98CA-2228977.
XX
XX 07-NOV-1997; 97CA-2215360.
XX
XX (EDEL/) EDELMAN E R.
XX (ROSE/) ROSENBERG R D.
XX (SIRO/) SIROIS M G.
XX (SIRO/) SIROIS M.
XX
XX Edelman ER, Rosenberg RD, Siros MG, Simons M;
XX WPI; 2000-283933/25.
XX
XX Antisense inhibition of platelet derived growth factor beta-receptor
XX subunit expression for the prevention of restenosis -
XX Claim 27; Page 23; 43pp; English.
XX
XX A method has been developed for preventing restenosis following vascular
XX injury by antisense inhibition of platelet derived growth factor
XX beta-receptor subunit (PDGFR-beta) expression. The method is used for
XX the prevention of restenosis (recurrent stenosis (narrowing of a duct or
XX canal), especially of a valve in the heart, after surgical correction of
XX the primary condition) following cardiovascular injury. The present

CC sequence represents a phosphorothioate antisense oligonucleotide for
 CC NMHC.

XX
 SQ Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 catgtctccacccttga 18
 ||||| ||||| ||||| |||||
 Db 1 catgtctccacccttga 18

RESULT 4

AAT43352
 ID AAT43352 standard; cDNA; 30 BP.

XX
 AC AAT43352;

DT 08-SEP-1997 (first entry)

XX Primer #1 for G-protein coupled receptor coding sequence.

XX G-protein coupled receptor; human; HIBEF51; transmembrane domain; ulcer;
 KW hormone; viral receptor; growth factor; neuroreceptor; neurotransmitter;
 KW signal transduction; central nervous system; hypertension; osteoporosis;
 KW angina pectoris; myocardial infarction; asthma; allergy; eating disorder;
 KW psychosis; depression; migraine; vomiting; stroke; cancer; hypotension;
 KW benign hypertrophy; Parkinson's disease; acute heart failure; therapy;
 KW urinary retention; primer; polymerase chain reaction; amplify; PCR; ss.

XX Synthetic.

XX WO9639441-A1.

XX 12-DEC-1996.

XX 06-JUN-1995; 95WO-US07225.

XX 06-JUN-1995; 95WO-US07225.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Adams MD, Li Y;

XX WPI; 1997-043076/04.

XX Human G-protein coupled receptor, HIBEF51 - used to identify
 PT (ant)agonists, used in the treatment of asthma, angina pectoris,
 PT psychotic and neurological disorders, and eating disorders etc.

XX Example 1; Page 35; 69pp; English.

XX AAT43352-T43357 represent primers for the coding sequence for the human
 CC G-protein coupled receptor HIBEF51 (see AAT43351 for amplified
 CC sequence). The protein encoded by the amplified sequence is a
 CC 7-transmembrane domain receptor. G-protein coupled receptors include a
 CC wide range of biologically active receptors, such as hormone, viral,
 CC growth factor and neuroreceptors. Most of the receptors have conserved
 CC cysteine residues in the first two extracellular loops, which form
 CC disulphide bonds thought to stabilise the functional protein structure.
 CC Phosphorylation or lipidation of these residues can influence the signal
 CC transduction of some G-protein coupled receptors. G-protein coupled
 CC receptors are found at numerous sites within a mammalian host, and some
 CC are critical neurotransmitters in the central nervous system. Compounds
 CC that activate or inhibit the receptor encoded by the amplified sequence
 CC may be used for the treatment of patients which need to activate or
 CC inhibit a G-protein coupled receptor. Mutations in the amplified sequence
 CC or the encoded protein may be identified by sequence analysis.
 CC Antagonists of the G-protein coupled receptor may be used for the
 CC treatment of hypertension, angina pectoris, myocardial infarction,

CC ulcers, asthma, allergies, psychoses, depression, migraine, vomiting,
 CC stroke, eating disorders, cancer and benign hypertrophy. Agonists of the
 CC protein may be used in the treatment of Parkinson's disease, acute heart
 CC failure, hypotension, urinary retention and osteoporosis.

XX Sequence 30 BP; 7 A; 10 C; 5 G; 8 T; 0 other;

Query Match 82.2%; Score 14.8; DB 18; Length 30;
 Best Local Similarity 88.9%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccacccttga 18
 ||||| ||||| ||||| |||||
 Db 12 catgaactccacccttga 29

RESULT 5

AAT43356
 ID AAT43356 standard; cDNA; 30 BP.

XX
 AC AAT43356;

XX 09-SEP-1997 (first entry)

XX Primer #5 for G-protein coupled receptor coding sequence.

XX G-protein coupled receptor; human; HIBEF51; transmembrane domain; ulcer;
 KW hormone; viral receptor; growth factor; neuroreceptor; neurotransmitter;
 KW signal transduction; central nervous system; hypertension; osteoporosis;
 KW angina pectoris; myocardial infarction; asthma; allergy; eating disorder;
 KW psychosis; depression; migraine; vomiting; stroke; cancer; hypotension;
 KW benign hypertrophy; Parkinson's disease; acute heart failure; therapy;
 KW urinary retention; primer; polymerase chain reaction; amplify; PCR; ss.

XX Synthetic.

XX WO9639441-A1.

XX 12-DEC-1996.

XX 06-JUN-1995; 95WO-US07225.

XX 06-JUN-1995; 95WO-US07225.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Adams MD, Li Y;

XX WPI; 1997-043076/04.

XX Human G-protein coupled receptor, HIBEF51 - used to identify
 PT (ant)agonists, used in the treatment of asthma, angina pectoris,
 PT psychotic and neurological disorders, and eating disorders etc.

XX Example 3; Page 38; 69pp; English.

XX AAT43352-T43357 represent primers for the coding sequence for the human
 CC G-protein coupled receptor HIBEF51 (see AAT43351 for amplified
 CC sequence). The protein encoded by the amplified sequence is a
 CC 7-transmembrane domain receptor. G-protein coupled receptors include a
 CC wide range of biologically active receptors, such as hormone, viral,
 CC growth factor and neuroreceptors. Most of the receptors have conserved
 CC cysteine residues in the first two extracellular loops, which form
 CC disulphide bonds thought to stabilise the functional protein structure.
 CC Phosphorylation or lipidation of these residues can influence the signal
 CC transduction of some G-protein coupled receptors. G-protein coupled
 CC receptors are found at numerous sites within a mammalian host, and some
 CC are critical neurotransmitters in the central nervous system. Compounds
 CC that activate or inhibit the receptor encoded by the amplified sequence
 CC may be used for the treatment of patients which need to activate or
 CC inhibit a G-protein coupled receptor. Mutations in the amplified sequence
 CC or the encoded protein may be identified by sequence analysis.

CC Antagonists of the G-protein coupled receptor may be used for the
CC treatment of hypertension, angina pectoris, myocardial infarction,
CC ulcers, asthma, allergies, psychoses, depression, migraine, vomiting,
CC stroke, eating disorders, cancer and benign hypertrophy. Agonists of the
CC protein may be used in the treatment of Parkinson's disease, acute heart
CC failure, hypotension, urinary retention and osteoporosis.
XX
SQ Sequence 30 BP; 6 A; 11 C; 6 G; 7 T; 0 other;

Query Match 82.2%; Score 14.8; DB 18; Length 30;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttggg 18
||||| ||||| ||||| |||||
Db 12 catgaactccaccttggg 29

RESULT 6
AAT43354
ID AAT43354 standard; cDNA; 34 BP.
XX
AC AAT43354;
XX
DT 09-SEP-1997 (first entry)
XX
DE Primer #3 for G-protein coupled receptor coding sequence.
XX
KW G-protein coupled receptor; human; HIBEF51; transmembrane domain; ulcer;
KW hormone; viral receptor; growth factor; neuroreceptor; neurotransmitter;
KW signal transduction; central nervous system; hypertension; osteoporosis;
KW angina pectoris; myocardial infarction; asthma; allergy; eating disorder;
KW psychoses; depression; migraine; vomiting; stroke; cancer; hypotension;
KW benign hypertrophy; Parkinson's disease; acute heart failure; therapy;
KW urinary retention; primer; polymerase chain reaction; amplify; PCR; ss.
XX
OS Synthetic.
XX
PN WO9639441-A1.
XX
PD 12-DEC-1996.
XX
PF 06-JUN-1995; 95WO-US07225.
XX
PR 06-JUN-1995; 95WO-US07225.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Adams MD, Li Y;
XX
WPI; 1997-043076/04.
XX
DR Human G-protein coupled receptor, HIBEF51 - used to identify
PT (antagonists, used in the treatment of asthma, angina pectoris,
PT psychotic and neurological disorders, and eating disorders etc.
XX
PS Example 2; Page 37; 69pp; English.
XX
CC AAT43352-T43357 represent primers for the coding sequence for the human
CC G-protein coupled receptor HIBEF51 (see AAT43351 for amplified
CC sequence). The protein encoded by the amplified sequence is a
CC 7-transmembrane domain receptor. G-protein coupled receptors include a
CC wide range of biologically active receptors, such as hormone, viral,
CC growth factor and neuroreceptors. Most of the receptors have conserved
CC cysteine residues in the first two extracellular loops, which form
CC disulphide bonds thought to stabilise the functional protein structure.
CC Phosphorylation or lipidation of these residues can influence the signal
CC transduction of some G-protein coupled receptors. G-protein coupled
CC receptors are found at numerous sites within a mammalian host, and some
CC are critical neurotransmitters in the central nervous system. Compounds
CC that activate or inhibit the receptor encoded by the amplified sequence
CC may be used for the treatment of patients which need to activate or

CC inhibit a G-protein coupled receptor. Mutations in the amplified sequence
CC or the encoded protein may be identified by sequence analysis.
CC Antagonists of the G-protein coupled receptor may be used for the
CC treatment of hypertension, angina pectoris, myocardial infarction,
CC ulcers, asthma, allergies, psychoses, depression, migraine, vomiting,
CC stroke, eating disorders, cancer and benign hypertrophy. Agonists of the
CC protein may be used in the treatment of Parkinson's disease, acute heart
CC failure, hypotension, urinary retention and osteoporosis.
XX
SQ Sequence 34 BP; 8 A; 12 C; 6 G; 8 T; 0 other;

Query Match 82.2%; Score 14.8; DB 18; Length 34;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttggg 18
||||| ||||| ||||| |||||
Db 16 catgaactccaccttggg 33

RESULT 7
AAA35676
ID AAA35676 standard; DNA; 36 BP.
XX
AC AAA35676;
XX
DT 26-JUL-2000 (first entry)
XX
DE Permutin linker encoding nucleotide sequence FGS101.
XX
KW Biologically-activated circularly-permuted protein; permutin; linker;
KW permutin library generation; therapeutic property; antigen;
KW immunotherapy; improve bio-distribution; half life; ss.
XX
OS Synthetic.
XX
PN WO200018905-A1.
XX
PD 06-APR-2000.
XX
PF 24-SEP-1999; 99WO-US20891.
XX
PR 25-SEP-1998; 98US-0101908.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Lee SC;
XX
WPI; 2000-293145/25.
XX
DR Preparation of biologically-activated circularly-permuted proteins by
PT scanning permutagenesis for generating libraries of permutins with
PT improved therapeutic properties -
XX
PS Claim 11; Page 41; 100pp; English.
XX
CC The preparation of biologically-activated circularly-permuted proteins
CC (permutins) comprises the use of a method comprising making a series of
CC circularly permuted genes. The circularly permuted genes are inserted
CC into a display vector, where they are expressed so that the proteins
CC they encode are presented on the surface of the display vector. A library
CC of display vectors presenting the expressed circularly permuted proteins
CC is generated. A target protein that can bind a biologically active
CC circularly permuted protein can be used to affinity select the
CC presenting display vectors. The selected circularly-permuted protein. The
CC and analysed to identify the structure of a parent protein consisting of a
CC permutin derived from the carboxy portion of the parent protein, a
CC segment derived from the amino terminus of the parent protein, and a
CC linker or chemical bond linking the amino and carboxy terminal derived
CC portions. Nucleotide sequences AAA35676-A35943 encode linkers used to
CC create the permutins of the invention. The method is used to generate

CC libraries of permuteins with improved therapeutic properties compared to
CC their parent molecules. Permutoins with little or no activity may be used
CC as antigens for producing antibodies which are used in immunology or
CC immunotherapy as probes or intermediates used to construct other useful
CC permutoins. Permutoins have improved biological and therapeutic
CC properties compared to their two individual components due to alterations
CC in bio-distribution or half-life.

XX SQ Sequence 36 BP; 7 A; 15 C; 8 G; 6 T; 0 other;

Query Match 82.2%; Score 14.8; DB 21; Length 36;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacccttggg 18
Db 9 catgtctccacccttggg 26
||||| |||||||

RESULT 8
AAT93540/C
ID AAT93540 standard; DNA; 41 BP.

XX AC AAT93540;

XX DT 19-FEB-1998 (first entry)

XX DE Antisense primer SK462 for amplification of QS RNA.

XX KW Armoured RNA; bacteriophage MS2; RT-PCR; ribonuclease; recombinant;
XX KW Human Immunodeficiency Virus; HIV; Hepatitis C Virus; HCV; viral RNA;
XX KW detection; quantification standard; maturase protein; coat protein;
XX KW PCR primer; QS RNA; reverse transcriptase-PCR; ss.

XX OS Synthetic.

XX OS Human Immunodeficiency Virus.

XX PN US5677124-A.

XX PD 14-OCT-1997.

XX PF 03-JUL-1996; 96US-0675153.

XX PR 03-JUL-1996; 96US-0675153.

XX PA (AMBI-) AMBION INC.

XX PA (CENE-) CENETRON DIAGNOSTICS LLC.

XX PI Dubois DB, Pasloske BL, Winkler MM;

XX DR WPI; 1997-511866/47.

XX PT Recombinant RNA segment encapsidated in bacteriophage viral coat
XX PT protein - RNA detection and/or quantification standard

XX PS Example 1; Column 15; 23pp; English.

XX CC This antisense primer is used in the RT-PCR amplification of QS RNA. The
XX CC QS RNA is used to construct an "armoured RNA" HIV standard PAR-2. An
XX CC "armoured RNA" is a recombinant RNA segment encapsidated in bacteriophage
XX CC viral coat protein. The recombinant RNA segment comprises an operator
XX CC coding sequence, a viral maturase protein binding site, and a non-
XX CC bacteriophage sequence. The QS sequence is the non bacteriophage HIV
XX CC standard in this case. The recombinant RNA in its packaged form is highly
XX CC resistant to ribonucleases, insuring that the RNA standard is not
XX CC compromised by inadvertent ribonuclease contamination. The armoured RNA
XX CC standards are ideal as RNA standards for the quantification of RNA
XX CC viruses such as HIV and HCV from human body fluids such as blood and
XX CC cerebrospinal fluid.

XX SQ Sequence 41 BP; 15 A; 7 C; 10 G; 9 T; 0 other;

Query Match 76.7%; Score 13.8; DB 18; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacccttggg 18
Db 24 ATGTCTCCCACTTAGA 8
||||| |||||||

RESULT 9
AAV18847/C

ID AAV18847 standard; DNA; 41 BP.

XX AC AAV18847;

XX DT 11-JUN-1998 (first entry)

XX DE Primer for QS RNA.

XX KW PCR primer; QS RNA; nucleic acid standard;
XX KW Armored RNA; ss.

XX OS Synthetic.

XX PN WO9800547-A1.

XX PD 08-JAN-1998.

XX PF 02-JUL-1997; 97WO-US12551.

XX PR 24-JUN-1997; 97US-0881571.

XX PR 03-JUL-1996; 96US-0021145.

XX PR 03-JUL-1996; 96US-0675153.

XX PA (AMBI-) AMBION INC.

XX PA (CENE-) CENETRON DIAGNOSTICS LLC.

XX PI Dubois DB, Pasloske BL, Winkler MM;

XX DR WPI; 1998-086972/08.

XX PT Ribonuclease resistant RNA molecules and their production - useful
XX PT as standards in quantitative PCR for pathogens, e.g HIV-1, HIV-2 and
XX PT HCV

XX PS Example 1; Page 32; 134pp; English.

XX CC The present sequence is a primer for QS RNA, which was used in the
XX CC preparation of a nucleic acid standard, comprising a nuclease
XX CC resistant nucleic acid segment encoding a standard nucleic acid,
XX CC i.e. RNA. The ribonuclease resistant RNA standard, designated
XX CC Armored RNA (RTM) is useful as an internal or external nucleic acid
XX CC standard in quantitative assays, e.g. PCR or RT-PCR for the
XX CC presence of a tested nucleic acid in blood samples.

XX SQ Sequence 41 BP; 15 A; 7 C; 10 G; 9 T; 0 other;

Query Match 76.7%; Score 13.8; DB 19; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacccttggg 18
Db 24 ATGTCTCCCACTTAGA 8
||||| |||||||

RESULT 10
AAV78449/C

ID AAV78449 standard; DNA; 41 BP.

XX AC AAV78449;

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XX DT 26-AUG-1999 (first entry)
XX DE HIV gag gene (QSRNA) PCR primer 2.
XX KW RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
XX KW Ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV;
XX KW HTLV-1; HTLV-2; hepatitis G; enterovirus; blood-borne pathogen; ss.
XX OS Synthetic.
XX OS Human immunodeficiency virus.
XX PN US5919625-A.
XX PD 06-JUL-1999.
XX PF 29-APR-1997; 97US-0841252.
XX PR 03-JUL-1996; 96US-0675153.
XX PR 29-APR-1997; 97US-0841252.
XX PA (AMBI-) AMBION INC.
XX PA (GENE-) CENTRON DIAGNOSTICS LLC.
XX PI Dubois DB, Pasloske BL, Winkler MW;
XX DR WPI; 1999-394617/33.
XX RW Ribonuclease resistant viral RNA standards
XX PT
XX PS Example 1; Column 29-30; 22pp; English.
XX CC This invention describes the construction of novel RNA standards for the
XX CC quantification of human immunodeficiency virus (HIV) and hepatitis C
XX CC virus (HCV) from e.g. cerebrospinal fluids. The method involves (1)
XX CC obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
XX CC RNA standard, encapsulated in a bacteriophage viral coat protein, which
XX CC comprises an RNA segment having a segment encoding a sequence that serves
XX CC as a standard in detection or quantification of the RNA of interest;
XX CC (3) mixing the sample with the standard; (4) isolating RNA from the
XX CC mixture, and (5) assaying for the presence of the RNA. The method is
XX CC useful for the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1,
XX CC HTLV-2, hepatitis G, an enterovirus, or a blood-borne pathogen. This
XX CC sequence represents a PCR primer used to amplify the HIV gag gene QSRNA
XX CC which is used in the method of the invention.
XX SQ Sequence 41 BP; 15 A; 7 C; 10 G; 9 T; 0 other;

Query Match 76.7%; Score 13.8; DB 20; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtcctccacccttggga 18
Db 24 ATGTCCTCCAACCTTAGA 8
||||||| ||| ||

RESULT 11
AAAF69745/C
ID AAF69745 standard; DNA; 23 BP.
XX AC AAF69745;
XX DT 18-APR-2001 (first entry)
XX DE Human IL4Ralpha gene PCR primer #81.
XX KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
XX KW allergic disease; PCR primer; ss.
XX OS Homo sapiens.
XX PI Winslow BJ, Cochran MD;

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PN WO200104270-A1.
XX 18-JAN-2001.
XX PF 13-JUL-2000; 2000WO-US19094.
XX PR 13-JUL-1999; 99US-0143435.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
XX PI Windemuth AK;
XX DR WPI; 2001-103078/11.
XX PS New isolated polynucleotide useful for the identification of
XX PT therapeutics in allergic diseases is new -
XX PS Example 1; Page 63; 188pp; English.
XX CC The present invention relates to polymorphisms of the human interleukin 4
XX CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
XX CC sequence). Polynucleotides comprising polymorphic gene variants are
XX CC useful for therapeutic purposes. For example, where a patient may benefit
XX CC from expression of a particular IL4Ralpha protein isoform, an expression
XX CC vector encoding the isoform may be administered to the patient. It may
XX CC desirable to decrease or block expression of a particular IL4Ralpha
XX CC isogene, which may be done by turning off by transforming a targeted
XX CC organ, tissue or cell population with an expression vector that expresses
XX CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
XX CC identified by these methods may be useful for allergic diseases. The
XX CC present sequence is a PCR primer for human IL4R-alpha.
XX SQ Sequence 23 BP; 10 A; 4 C; 7 G; 2 T; 0 other;

Query Match 74.4%; Score 13.4; DB 22; Length 23;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 catgtcctccacctt 15
Db 16 CATGTCCTCTACCTT 2
||||||| |||||

RESULT 12
AAZ34849
ID AAZ34849 standard; DNA; 20 BP.
XX AC AAZ34849;
XX DT 28-FEB-2000 (first entry)
XX DE Feline CTLA-4 3' PCR primer.
XX KW CTLA-4; feline; cat; recombinant virus; vaccine; immunomodulator;
XX KW tumour; cancer; therapy; PCR; primer; ss.
XX OS Synthetic.
XX OS Felis domesticus.
XX PN WO9957295-A1.
XX PD 11-NOV-1999.
XX PF 30-APR-1999; 99WO-US09504.
XX PR 01-MAY-1998; 98US-0071711.
XX PA (SCHE ) SCHERING-PLOUGH LTD.
XX PA (SCHE ) SCHERING-PLOUGH VETERINARY CORP.
XX PI Winslow BJ, Cochran MD;

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XX WPI; 2000-062155/05.
XX Novel recombinant virus useful as immunomodulators, particularly in
XX vaccines -
XX
XX Example 1A; Page 73; 230pp; English.
XX
XX This oligonucleotide represents a 3' primer used in a nested-PCR
XX amplification of feline CTLA-4 cDNA (see AA234840). The invention
XX relates to a recombinant virus that contains at least one foreign
XX nucleic acid, inserted into a nonessential genomic region, that
XX encodes feline CD80, CD86 or CTLA-4 protein, or their
XX immunogenic fragments, and is expressed when the recombinant
XX virus is introduced into a suitable host. The recombinant virus
XX may further comprise a foreign nucleic acid encoding an immunogen
XX derived from a feline pathogen. It is used to enhance or suppress
XX an immune response in a feline, particularly as a vaccine.
XX
XX Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 other;

Query Match      73.3%; Score 13.2; DB 21; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtcctccaccttga 18
Db 11111111111111111111
2 catgagctccaccttga 19

RESULT 13
AAZ34797
ID AA234797 standard; DNA; 20 BP.
XX
XX AAZ34797;
XX
XX 15-FEB-2000 (first entry)
XX
XX Cat CTLA-4 receptor cDNA 3' PCR primer.
XX
XX CTLA-4; CD152; receptor; cat; vaccine; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Felis domesticus.
XX
XX WO9957271-A2.
XX
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09502.
XX
XX 01-MAY-1998; 98US-0071699.
XX
XX (TEXA ) TEXAS A & M SYSTEM.
XX
XX Collison EW, Hash SM, Choi I;
XX
XX WPI; 2000-052972/04.
XX
XX Novel feline proteins used to produce feline vaccines which prevent
XX infectious disease or to promote growth in homologous or heterologous
XX species -
XX
XX Example 1A; Page 38; 186pp; English.
XX
XX This oligonucleotide represents a 3' primer used in nested PCR
XX amplification of feline CTLA-4 (CD152) receptor 5' region cDNA (see
XX AA234787). The template was the product of a first PCR amplification
XX of peripheral blood mononuclear cell cDNA. The invention provides
XX nucleic acids encoding feline CD80 ligand, feline CD86 (B7-2)
XX ligand, feline CD28 receptor or feline CTLA-4 receptor, as well as
XX vectors comprising the nucleic acids, and polypeptides encoded by

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CC the nucleic acids. It also provides vaccines comprising the CD80,
CC CD86, CD28 or CTLA-4 polypeptides and further comprising immunogens
CC derived from pathogens, as well as vaccines capable of enhancing an
CC immune response and vaccines capable of suppressing an immune
CC response.
XX
XX Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 other;

Query Match      73.3%; Score 13.2; DB 21; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtcctccaccttga 18
Db 11111111111111111111
2 catgagctccaccttga 19

RESULT 14
AAH19003
ID AAH19003 standard; DNA; 24 BP.
XX
XX AAH19003;
XX
XX 21-JUN-2001 (first entry)
XX
XX Reverse primer used to amplify UCP3 gene promoter region 1.
XX
XX UCP3; uncoupling protein 3; polymorphism; obesity;
XX diabetes mellitus; ss.
XX
XX Homo sapiens.
XX
XX WO200118232-A2.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-US24784.
XX
XX 08-SEP-1999; 99US-0152789.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX (STEP/) STEPHENS J C.
XX
XX Chew A, Choi JY, Denton RR, Nandabalan K;
XX
XX WPI; 2001-218562/22.
XX
XX Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
XX carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
XX useful for the design of drugs for treating obesity -
XX
XX Example 1; Page 33; 94pp; English.
XX
XX The present invention relates to the human uncoupling protein 3
XX (mitochondrial, proton carrier) (UCP3) gene and polymorphisms.
XX The polymorphisms are associated with obesity, especially
XX diabetes mellitus associated obesity. They polymorphisms may be
XX identified and analysed to determine whether an individual is
XX susceptible to obesity and may be used as the basis for targeted
XX design of drugs to treat obesity. The present sequence was used in
XX the identification and amplification of UCP3 polymorphisms.
XX
XX Sequence 24 BP; 2 A; 9 C; 4 G; 9 T; 0 other;

Query Match      73.3%; Score 13.2; DB 22; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtcctccaccttga 18
Db 11111111111111111111
5 cctgtcctctctcttga 22

```

```
RESULT 15
AAH19025
ID AAH19025 standard; DNA; 24 BP.
XX
AC AAH19025;
XX
DT 21-JUN-2001 (first entry)
XX
DE Reverse primer used to sequence UCP3 gene promoter region 1.
XX
KW UCP3; uncoupling protein 3; polymorphism; obesity;
KW diabetes mellitus; ss.
XX
OS Homo sapiens.
XX
PN WO200118232-A2.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-US24784.
XX
PR 08-SEP-1999; 99US-0152789.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (STEP/) STEPHENS J C.
XX
PI Chew A, Choi JY, Denton RR, Nandabalan K;
XX
DR WPI; 2001-218562/22.
XX
XX
XX Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
PT useful for the design of drugs for treating obesity -
XX
XX Example 1; Page 35; 94pp; English.
XX
XX The present invention relates to the human uncoupling protein 3
CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms.
CC The polymorphisms are associated with obesity, especially
CC diabetes mellitus associated obesity. They polymorphisms may be
CC identified and analysed to determine whether an individual is
CC susceptible to obesity and may be used as the basis for targeted
CC design of drugs to treat obesity. The present sequence was used in
CC the identification and amplification of UCP3 polymorphisms.
XX
SQ Sequence 24 BP; 2 A; 9 C; 4 G; 9 T; 0 other;
```

Query Match 73.3%; Score 13.2; DB 22; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catgtctctccaccttggga 18
| | | | | | | | | |
Db 5 cctgtctctcttcttggga 22

Search completed: October 12, 2002, 17:08:04
Job time: 9749 sec

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:37 ; Search time 191.26 Seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-6

Perfect score: 18

Sequence: 1 catgtccctccaccttggga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCRUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
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2	18	100.0	18	5	PCT-US92-00626-2
3	14.8	82.2	30	2	US-08-465-971B-5
4	14.8	82.2	30	2	US-08-465-971B-9
5	14.8	82.2	34	2	US-08-465-971B-7
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C 11	13.2	73.3	30	3	US-08-505-058-12
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C 13	13.2	73.3	30	4	US-09-455-679-17
C 14	13.2	73.3	30	4	US-09-455-679-17
C 15	12.8	71.1	25	3	US-09-255-912-4
C 16	12.8	71.1	28	2	US-08-859-998-888
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C 26	12.4	68.9	50	1	US-08-207-901-34
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C 28	12.2	67.8	45	1	US-08-208-886C-30
C 29	12.2	67.8	45	1	US-08-704-744-30
C 30	12.2	67.8	45	1	US-08-469-557-30
C 31	12.2	67.8	45	2	US-08-290-793B-30
C 32	12.2	67.8	47	2	US-08-687-355A-19
C 33	12.2	67.8	47	2	US-08-687-355A-20
C 34	12	66.7	30	1	US-08-384-708A-180
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C 36	12	66.7	31	3	US-08-795-430-20
C 37	11.8	65.6	20	3	US-08-889-108-6
C 38	11.8	65.6	20	4	US-08-120-601B-6
C 39	11.8	65.6	20	5	PCT-US94-10358-6
C 40	11.8	65.6	21	4	US-09-226-012-77
C 41	11.8	65.6	24	2	US-08-190-199A-48
C 42	11.8	65.6	40	1	US-07-872-673B-18
C 43	11.8	65.6	48	2	US-08-190-199A-53
C 44	11.8	65.6	48	2	US-08-729-955A-9
C 45	11.8	65.6	48	4	US-09-425-638A-28

ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/08369282
; Patent No. 5593974
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, ROBERT D
; APPLICANT: SIMONS, MICHAEL
; APPLICANT: EDELMAN, ELAZER
; APPLICANT: LANGER, ROBERT S
; APPLICANT: DEKEYSER, JEAN-LUC
; TITLE OF INVENTION: LOCALIZED OLIGONUCLEOTIDE THERAPY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,282
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/855,416
; FILING DATE:
; APPLICATION NUMBER: US 792,146
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 723,454
; FILING DATE: 28-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MIT5583CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /standard_name= "ANTISENSE HUMAN
; OTHER INFORMATION: NMHC"
; OTHER INFORMATION: /note= "ANTISENSE SEQUENCE TO HUMAN NMHC"
US-08-369-282-2

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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CATGTCTCCACCTTGA 18

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; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, ROBERT D
; APPLICANT: SIMONS, MICHAEL
; APPLICANT: EDELMAN, ELAZER
; APPLICANT: LANGER, ROBERT S
; APPLICANT: DEKEYSER, JEAN-LUC
; TITLE OF INVENTION: LOCALIZED OLIGONUCLEOTIDE THERAPY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION NUMBER: PCT/US92/00626
; FILING DATE: 19921105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 792,146
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 723,454
; FILING DATE: 28-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MIT5583CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /standard_name= "ANTISENSE HUMAN
; OTHER INFORMATION: NMHC"
; OTHER INFORMATION: /note= "ANTISENSE SEQUENCE TO HUMAN NMHC"

PCT-US92-00626-2

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 5, Application US/08465971B
; Patent No. 5942414
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,971B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-465-971B-5

Query Match 82.2%; Score 14.8; DB 2; Length 30;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 12 CATGAACCTCCACCTTGA 29

RESULT 4
US-08-465-971B-9
; Sequence 9, Application US/08465971B
; Patent No. 5942414
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-465-971B-9

Query Match 82.2%; Score 14.8; DB 2; Length 30;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 12 CATGAACCTCCACCTTGA 29

RESULT 5
US-08-465-971B-7
Sequence 7, Application US/08465971B
Patent No. 5942414
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-465-971B-7

Query Match 82.2%; Score 14.8; DB 2; Length 34;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctctccaccttggg 18
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Db 16 CATGAACCTCCACCTTGA 33

RESULT 6
US-08-675-153-5/c
Sequence 5, Application US/08675153
Patent No. 5677124
GENERAL INFORMATION:
APPLICANT: DuBois, Dwight
APPLICANT: Winkler, Matthew
APPLICANT: Pasloske, Brittan L.
TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
TITLE OF INVENTION: RNA STANDARDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,153
FILING DATE: Concurrently Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AMBI:026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-675-153-5

Query Match 76.7%; Score 13.8; DB 1; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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US-08-841-252-5/c

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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,571
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/675,153
FILING DATE: 03-JUL-1996
PRIOR APPLICATION DATA: US 60/021,145
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AMBT:033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-571-5

Query Match 76.7%; Score 13.8; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 3,1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels

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Db 24 ATGCTCTCCAACHTAGA 8

RESULT 9
US-09-282-054-5/c
Sequence 5, Application US/09282054
Patent No. 6214982
GENERAL INFORMATION:
APPLICANT: Pasloske, Brittan L.
APPLICANT: DuBois, Dwight
APPLICANT: Brown, David
APPLICANT: Winkler, Matthew
TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
TITLE OF INVENTION: AND UTILIZATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,054
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/881,571
FILING DATE:
APPLICATION NUMBER: US 08/675,153
FILING DATE: 03-JUL-1996
PRIOR APPLICATION DATA:

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; EARLIER FILING DATE: 1997-08-06
 ; EARLIER APPLICATION NUMBER: 60/054,867
 ; EARLIER FILING DATE: 1997-08-06

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; OTHER INFORMATION: Primer
US-09-455-679-17

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 26 cagtcgcgcaccttgg 43

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; Sequence 4, Application US/09255912
; Patent No. 6037142
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTS-0044
; CURRENT APPLICATION NUMBER: US/09/255,912
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-255-912-4

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Best Local Similarity 87.5%; Pred. No. 8.8e+02;
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; Sequence 16, Application US/09455679
; Patent No. 6329186
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Svendsen, Allan
; APPLICANT: Boisen, Kirsten
; APPLICANT: Vind, Jesper
; APPLICANT: Pedersen, Henrik
; TITLE OF INVENTION: Glucoamylases With N-Terminal Extensions
; FILE REFERENCE: 5691.200-US
; CURRENT APPLICATION NUMBER: US/09/455,679
; CURRENT FILING DATE: 1999-12-07
; EARLIER APPLICATION NUMBER: PA 1998 01616
; EARLIER FILING DATE: 1998-12-07
; EARLIER APPLICATION NUMBER: PA 1999 00409
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/111,674
; EARLIER FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/126,740
; EARLIER FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-455-679-16

Query Match      73.3%; Score 13.2; DB 4; Length 50;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catgtctccaccttgg 18
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Db 26 cagtcgcgcaccttgg 43

RESULT 14
US-09-455-679-17
; Sequence 17, Application US/09455679
; Patent No. 6329186
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Svendsen, Allan
; APPLICANT: Boisen, Kirsten
; APPLICANT: Vind, Jesper
; APPLICANT: Pedersen, Henrik
; TITLE OF INVENTION: Glucoamylases With N-Terminal Extensions
; FILE REFERENCE: 5691.200-US
; CURRENT APPLICATION NUMBER: US/09/455,679
; CURRENT FILING DATE: 1999-12-07
; EARLIER APPLICATION NUMBER: PA 1998 01616
; EARLIER FILING DATE: 1998-12-07
; EARLIER APPLICATION NUMBER: PA 1999 00409
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/111,674
; EARLIER FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/126,740
; EARLIER FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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13	18	100.0	18	6	AX283213	AX283213 Sequence
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15	18	100.0	18	6	I33927	I33927 Sequence 5
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c 22	13.4	74.4	30	6	AR048612	AR048612 Sequence
23	13.4	74.4	37	6	AX179598	AX179598 Sequence
24	13.2	73.3	18	6	AR034550	AR034550 Sequence
c 25	13.2	73.3	39	6	AR021477	AR021477 Sequence
c 26	13.2	73.3	39	6	AR061315	AR061315 Sequence
c 27	13.2	73.3	39	6	AR100113	AR100113 Sequence
c 28	13.2	73.3	39	6	AR175970	AR175970 Sequence
29	13	72.2	24	6	AX298054	AX298054 Sequence
30	12.8	71.1	27	6	AR146809	AR146809 Sequence
c 31	12.8	71.1	46	6	AR082248	AR082248 Sequence
c 32	12.8	71.1	46	6	AR082271	AR082271 Sequence
c 33	12.8	71.1	46	6	AR120790	AR120790 Sequence
c 34	12.8	71.1	46	6	AR120813	AR120813 Sequence
c 35	12.8	71.1	46	6	I78294	I78294 Sequence 92
c 36	12.8	71.1	46	6	I78317	I78317 Sequence 11
c 37	12.4	68.9	38	6	AR119237	AR119237 Sequence
c 38	12.4	68.9	39	6	AR119238	AR119238 Sequence
c 39	12.4	68.9	39	6	AX031333	AX031333 Sequence
c 40	12.2	67.8	18	6	AR009808	AR009808 Sequence
c 41	12.2	67.8	20	6	AR009488	AR009488 Sequence
c 42	12.2	67.8	20	6	AR064146	AR064146 Sequence
c 43	12.2	67.8	20	6	AX296440	AX296440 Sequence
c 44	12.2	67.8	20	6	I35567	I35567 Sequence 14
45	12.2	67.8	23	6	AR009489	AR009489 Sequence

ALIGNMENTS

RESULT 1	A42368	A42368	18 bp	DNA	linear	PAT 05-MAR-1997
LOCUS	Sequence 28 from Patent WO9501363.					
DEFINITION	A42368					
ACCESSION	A42368.1	GI:2297844				
VERSION						
KEYWORDS	unidentified.					
SOURCE	unclassified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 18)					
AUTHORS	Uhlmann,E. and Meier,C.					
TITLE	METHYLPHOSPHONIC ACID ESTER, PROCESS FOR PREPARING THE SAME AND ITS					
JOURNAL	US					
COMMENT	Patent: WO 9501363-A 28 12-JAN-1995; HOECHST AG (DE) Other publication FI 956341 960219 Other publication CA 2165971 950112 Other publication NO 955352 960214 Other publication AU 7073594 950124 Other publication DE 4321946 950112.					
FEATURES	Location/Qualifiers					
source	1..18					

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 6
AR034535/c
LOCUS AR034535 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 38 from patent US 5869462.
ACCESSION AR034535
VERSION AR034535.1 GI:5950140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5869462-A 38 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
BASE COUNT 3 a 5 c 5 g 5 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 7
AR034536
LOCUS AR034536 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 39 from patent US 5869462.
ACCESSION AR034536
VERSION AR034536.1 GI:5950141
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5869462-A 39 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
BASE COUNT 5 a 5 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGGCGTGCCTCAAA 18

RESULT 8
AR048614
LOCUS AR048614 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5821234.

ACCESSION AR048614
VERSION AR048614.1 GI:5970957
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5821234-A 17 13-OCT-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
BASE COUNT 5 a 5 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGGCGTGCCTCAAA 18

RESULT 9
AR048616/c
LOCUS AR048616 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5821234.
ACCESSION AR048616
VERSION AR048616.1 GI:5970959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5821234-A 19 13-OCT-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
BASE COUNT 3 a 5 c 5 g 5 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 10
AR048635/c
LOCUS AR048635 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 38 from patent US 5821234.
ACCESSION AR048635
VERSION AR048635.1 GI:5970978
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5821234-A 38 13-OCT-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

```

BASE COUNT      3 a      5 c      5 g      5 t
ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 18 GATCAGCGGTGCCTCAAA 1

RESULT 11
AR048636
LOCUS      18 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 39 from patent US 5821234.
ACCESSION AR048636
VERSION AR048636.1 GI:5970979
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau,V.J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5821234-A 39 13-OCT-1998;
FEATURES
source 1..18
BASE COUNT      5 a      5 c      5 g      3 t
ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 18

RESULT 12
AX081383
LOCUS      18 bp      DNA      linear      PAT 27-FEB-2001
DEFINITION Sequence 62 from Patent WO0108707.
ACCESSION AX081383
VERSION AX081383.1 GI:13170225
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
TITLE Conjugates and methods for the production thereof, and their use
for transporting molecules via biological membranes
JOURNAL Patent: WO 0108707-A 62 08-FEB-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:
Oligonukleotide"
BASE COUNT      5 a      5 c      5 g      3 t
ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 18

RESULT 13
AX283213
LOCUS      18 bp      DNA      linear      PAT 20-NOV-2001
DEFINITION Sequence 51 from Patent WO0179216.
ACCESSION AX283213
VERSION AX283213.1 GI:17044094
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (sites)
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing them
JOURNAL Patent: WO 0179216-A 51 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Oligonukleotide"
BASE COUNT      5 a      5 c      5 g      3 t
ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 18

RESULT 14
AX283283
LOCUS      18 bp      DNA      linear      PAT 20-NOV-2001
DEFINITION Sequence 47 from Patent WO0179249.
ACCESSION AX283283
VERSION AX283283.1 GI:17044164
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (sites)
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing the same
JOURNAL Patent: WO 0179249-A 47 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:
Oligonukleotide"
BASE COUNT      5 a      5 c      5 g      3 t
ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 18
```


RESULT 15
I33927
LOCUS I33927 18 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 5 from patent US 5593974.
ACCESSION I33927
VERSION I33927.1 GI:1824718
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rosenberg,R.D., Simons,M., Edelman,E., Langer,R.S. and
DeKeyser,J.-L.
TITLE Localized oligonucleotide therapy
JOURNAL Patent: US 5593974-A 5 14-JAN-1997;
FEATURES
 source
 1..18
 /organism="unknown"
BASE COUNT 5 a 5 c 5 g 3 t
ORIGIN

Query Match . 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
 |||||
Db 1 GATCAGCGTGCCCTCAA 18

Search completed: October 12, 2002, 16:51:20
Job time: 8895 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:04 ; Search time 792.17 seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-7

Perfect score: 18

Sequence: 1 gatcaggcgctgcctcaaa 18

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	14	AAQ42221
2	18	100.0	18	14	AAQ35160
3	18	100.0	18	16	AAT44447
4	18	100.0	18	16	AAQ75057
5	18	100.0	18	16	AAQ75059
6	18	100.0	18	16	AAQ75079
7	18	100.0	18	16	AAQ88735
8	18	100.0	18	17	AAT37345
9	18	100.0	18	17	AAT51718

10	18	100.0	18	17	AAT39739
11	18	100.0	18	21	AAAL3833
12	18	100.0	18	22	AAF60953
13	18	100.0	18	22	AAH49236
14	18	100.0	18	24	ABL01645
15	18	100.0	27	14	AAQ37751
16	15	83.3	30	16	AAT05427
17	13.4	74.4	30	16	AAQ75055
18	13.4	74.4	37	22	AAQ09734
19	13.2	73.3	37	22	AAQ37348
20	13.2	73.3	34	19	AAV36244
21	13.2	73.3	39	19	AAV42360
22	13.2	73.3	39	20	AAV81347
23	13.2	73.3	39	21	AAE62334
24	13.2	73.3	39	24	AAE17270
25	13	72.2	24	24	AAE19121
26	12.8	71.1	27	19	AAV26324
27	12.8	71.1	27	20	AAE26071
28	12.8	71.1	27	21	AAZ87557
29	12.8	71.1	27	22	AAE03974
30	12.8	71.1	46	16	AAQ83065
31	12.8	71.1	46	16	AAQ83042
32	12.4	68.9	38	20	AAE25748
33	12.4	68.9	38	20	AAE21594
34	12.4	68.9	38	20	AAE21590
35	12.4	68.9	38	20	AAE16068
36	12.4	68.9	39	18	AAE8531
37	12.4	68.9	39	20	AAE84376
38	12.4	68.9	39	20	AAE25749
39	12.4	68.9	39	20	AAE21595
40	12.4	68.9	39	20	AAE21591
41	12.4	68.9	39	20	AAE16069
42	12.2	67.8	18	14	AAQ37745
43	12.2	67.8	18	19	AAV30104
44	12.2	67.8	20	16	AAQ87332
45	12.2	67.8	20	21	AAZ49018

ALIGNMENTS

RESULT	1
AAQ42221	
ID	AAQ42221 standard; DNA; 18 BP.
XX	AAQ42221;
AC	AAQ42221;
XX	
DT	02-SEP-1993 (first entry)
XX	
DE	Antisense sequence to PCNA.
XX	
KW	Antisense; oligonucleotide; inhibit; translation; transcription;
KW	target; nucleic acid; mammal; tissue; hybridise; combine; carrier;
KW	polyethylene oxide; polypropylene oxide; copolymer; ss.
XX	
OS	Synthetic.
XX	
PN	WO9308845-A.
XX	
PD	13-MAY-1993.
XX	
PF	05-NOV-1992; 92WO-US09626.
XX	
PR	08-NOV-1991; 91US-0792146.
PR	18-MAR-1992; 92US-0855416.
XX	(MASI) MASSACHUSETTS INST TECHNOLOGY.
PI	Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
PI	Simons M;
XX	
DR	WPI; 1993-167406/20.
XX	

PT Inhibiting translation or transcription of target nucleic acid -
PT by local administration in vivo of oligo:nucleotide complementary
to target sequence
XX
PS Disclosure; Page 41; 65pp; English.
XX
CC The sequences given in AAQ42217-21 are antisense oligonucleotides
CC which were used to inhibit translation or transcription of target
CC nucleic acids at a locus in vivo. The oligonucleotide are applied
CC directly to a tissue at the locus within the body of a mammal and
CC they are able to penetrate the cells of the tissue, hybridise/combine
CC with the target nucleic acid inhibiting intracellular translation or
CC transcription. The oligonucleotide are incorporated into a carrier
XX eg. a polyethylene oxide-polypropylene oxide copolymer.
XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gatcaggcgtgcctcaaa 18
|||||
DB 1 gatcaggcgtgcctcaaa 18

RESULT 2
AAQ35160
ID AAQ35160 standard; DNA; 18 BP.
XX AC
XX AC
XX AC
XX AAQ35160;
XX
XX 02-JUN-1993 (first entry)
XX
XX PCNA antisense oligonucleotide.
XX
XX Antisense; inhibit; protein coding genes; regulatory DNA; stroke;
XX endonuclease; vascular restenosis; myocardial infarction; embolism;
XX peripheral muscular disease; peripheral angioplasty; thrombophlebitis;
XX vasculitis; angina; Budd-Chiari syndrome; thrombosis; atherosclerosis;
XX hypertension; primary pulmonary; proliferative glomerulonephritis;
XX acute respiratory distress syndrome; idiopathic pulmonary fibrosis;
XX emphysema; ss.
XX
XX Synthetic.
XX
XX WO9301286-A.
XX
XX 21-JAN-1993.
XX
XX 23-JUN-1992; 92WO-US05305.
XX
XX 28-JUN-1991; 91US-0723454.
XX
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
XX Simons M,
XX
XX WPI; 1993-045491/05.
XX
XX Localised therapy using anti-sense oligo:nucleotide(s) - which
XX penetrate through tissue cell to hybridise with target m-RNA and
XX inhibit expression of the gene, for treatment of vascular
XX disorders, atherosclerosis, hypertension, etc.
XX
XX Example 4; Page 33; 59pp; English.
XX
XX The sequences given in AAQ34766-67 and AAQ35258-60 are antisense
XX oligonucleotides which were used in a method of inhibiting a target
XX nucleic acid sequence. The method may be used for inhibiting the
XX expression of protein coding genes as well as regulatory DNA.

CC Application of the antisense oligonucleotides to a defined locus in
CC vivo allows their use when systemic administration is not possible,
CC ie. sytemically administered oligos may be rendered inefficient by
CC endonucleases before they reach their targets. This method may be
CC used in the treatment of vascular disorders, particularly vascular
CC restenosis, myocardial infarction, peripheral muscular disease;
CC peripheral angioplasty, thrombophlebitis, stroke, embolism,
CC vasculitis, angina, Budd-Chiari syndrome, thrombosis, atherosclerosis,
CC hypertension, primary pulmonary hypertension, proliferative glomerulo-
CC nephritis, acute respiratory distress syndrome, idiopathic pulmonary
CC fibrosis or emphysema.
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
XX
Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gatcaggcgtgcctcaaa 18
|||||
DB 1 gatcaggcgtgcctcaaa 18

RESULT 3
AAT44447
ID AAT44447 standard; DNA; 18 BP.
XX AC
XX AAT44447;
XX
XX 27-JAN-1997 (first entry)
XX
XX Antisense oligonucleotide against PCNA gene.
XX
XX 8-azapurine; modification; stronger complex; inhibition;
XX proliferating cell nuclear antigen; ss.
XX
XX Synthetic.
XX
XX EP680969-A2.
XX
XX 08-NOV-1995.
XX
XX 26-APR-1995; 95EP-0106230.
XX
XX 02-MAY-1994; 94DE-4415370.
XX
XX (FARH) HOECHST AG.
XX
XX Lampe S, Seela F;
XX
XX WPI; 1995-375165/49.
XX
XX New oligo:nucleotide(s) contg. 8-aza:purine base - useful as
XX therapeutic and diagnostic agents with more stable hybridisation to
XX target nucleic acid
XX
XX Disclosure; Page 43; 51pp; German.
XX
XX AAT44425-54 are antisense oligonucleotides which have at least one
XX 8-azapurine base. The presence of an 8-azapurine base results in
XX significantly stronger complexing when hybridising to target nucleic
XX acids. The present sequence is against proliferating cell nuclear
XX antigen (PCNA) gene.
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
XX
Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gatcaggcgtgcctcaaa 18

PT kinase genes, partic. for preventing restenosis after
PT cardiovascular angioplasty.

XX
PS Disclosure; Page 13; 77pp; English.

XX
CC AAQ75079 is a rat proliferative cell nuclear antigen (PCNA) antisense
CC oligomer, which inhibits the expression of PCNA. When administered
CC to a site of lesion formation the antisense oligomer helps prevent
CC restenosis, after cardiovascular angioplasty.

XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgctgctcaaa 18
Db 1 gatcaggcgctgctcaaa 18

RESULT 7

AAQ88735
ID AAQ88735 standard; DNA; 18 BP.

XX
AC AAQ88735;

XX
DT 27-FEB-1996 (first entry)

XX
DE Human PCNA modified antisense oligonucleotide.

XX
KW antisense; analogue; non-terminal pyrimidine; phosphorothioate;
KW backbone; treatment; HIV; human immunodeficiency virus; HSV;
KW herpes simplex virus; cancer; integrin; cell adhesion receptor;
KW infection; diagnosis; nuclease resistance; ss.

XX
OS Homo sapiens.

XX
PN EP653439-A2.

XX
PD 17-MAY-1995.

XX
PF 07-NOV-1994; 94EP-0117513.

XX
PR 12-NOV-1993; 93DE-4338704.

XX
PA (FARH) HOECHST AG.

XX
PI Helsing M, Kretzschmar G, Mag M, Peyman A, Uhlmann E;
PI Winkler I;

XX
WPI; 1995-180677/24.

XX
PT New anti-sense oligo:nucleotide analogues - with modified
PT non-terminal pyrimidine nucleotide units, useful for treating viral
PT infections, cancer, etc.

XX
PS Claim 1; Page 29; 36pp; German.

XX
CC The antisense oligonucleotide (ON) shown is a derivative of an
CC equivalent wild type Human proliferating cell nuclear antigen ON, in
CC which at least one, esp. 2-10, non-terminal pyrimidine nucleotide(s)
CC is/are modified. The modification may be: (a) replacement of a
CC phosphodiester linkage by: a phosphorothioate (PS), -dithioate,
CC -aramidate; borano-, alkyl-, aralkyl-phosphate; 2,2,2-trichloro-1,1
CC -dimethyl-, alkyl- or aryl- phosphonate linkage; or (3'-thio)formacetal,
CC methylhydroxylamine, oxime, methylenedimethylhydrazo, dimethylene sulphone
CC or silyl linkage; (b) replacement of a sugar phosphate backbone by a
CC 'morpholinonucleoside' oligomer; (c) replacement of beta-D-2-deoxyribose
CC by another sugar or carbocyclic, open-chain or bicyclic sugar analogue;
CC or (c) replacement of the natural nucleoside base by an analogue, e.g.
CC 5-hydroxymethyl-uridine. The 5' and/or 3' terminus may also be modified

CC with a lipophilic gp., eg. a farnesyl. The modifications increase
CC nuclease resistance and thus improve stability and activity.

XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgctgctcaaa 18
Db 1 gatcaggcgctgctcaaa 18

RESULT 8

AAT37345
ID AAT37345 standard; DNA; 18 BP.

XX
AC AAT37345;

XX
DT 02-MAY-1997 (first entry)

XX
DE Oligonucleotide antisense to human PCNA position 4 to 22.

XX
KW Antisense; cyclin; cyclin dependent kinase; inhibition;
KW vascular lesion; mammary; carotid artery; femoral artery;
KW renal artery; renal dialysis fistula; cardiovascular angioplasty;
KW vein grafting; ss.

XX
OS Synthetic.

XX
PN WO9625491-A2.

XX
PD 22-AUG-1996.

XX
PF 15-FEB-1996; 96WO-US02064.

XX
PR 16-FEB-1995; 95US-0389926.

XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX
PI Dzaou VJ;

XX
WPI; 1996-393393/39.

XX
PT Inhibition of vascular lesion formation - by treatment with an
PT anti-sense oligomer to a gene expressing a cyclin or cyclin
PT dependent kinase.

XX
PS Example 6; Page 54; 76pp; English.

XX
CC The sequences given in AAT37343-46 represent oligonucleotides which are
CC antisense, with some mismatch base pairs, to the proliferating cell
CC nuclear antigen and cdc2 genes. The antisense oligomers may be used for
CC inhibiting vascular lesion formation in mammals, such as lesions in
CC the carotid, femoral and renal arteries, particularly lesions
CC resulting from renal dialysis fistula. They are particularly useful
CC in treating vascular lesions associated with cardiovascular
CC angioplasty. They can also be used in vein grafting. The antisense
CC oligomers may be directed against cyclin A, B1, B2, C, D1, D2, D3, E
CC or cyclin X (p46) or cyclin dependent kinase cdc 2, cdk 2, cdk 4
CC or cdk 5. They are preferably used with other agents e.g.
CC N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethylammonium chloride.

XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgctgctcaaa 18

```

Db      1 gatcaggcgtgcctcaaa 18
|||||
RESULT 9
AAT51718
ID      AAT51718 standard; DNA; 18 BP.
XX
AC      AAT51718;
XX
XX      09-APR-1997 (first entry)
DT
DE
DE      Oligonucleotide 2342.
XX
KW      Antisense oligonucleotide; rat; cdc gene; lipid complex; restenosis;
KW      aminomannose derivatised cholesterol; vascular smooth muscle; liposome;
KW      cell-cycle regulatory gene; proliferating cell nuclear antigen; PTCA;
KW      inhibitor; neointima hyperplasia; angioplasty injury; PCNA;
KW      percutaneous transluminal coronary angioplasty; ss.
XX
OS      Synthetic.
XX
PN      WO9624333-A1.
XX
PD      15-AUG-1996.
XX
PF      09-FEB-1996; 96WO-US01807.
XX
PR      10-FEB-1995; 95US-0386579.
XX
PA      (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI      Male-Brunne R;
XX
DR      WPI; 1996-384195/38.
XX
PT      Vascular targeting of therapeutic or imaging agents - using
PT      liposome(s) contg. amino:mannose-derivatised cholesterol
XX
PS      Example 2; Page 17; 45pp; English.
XX
CC      This sequence represents an antisense oligonucleotide that targets the
CC      rat proliferating cell nuclear antigen (PCNA) gene. This sequence is
CC      complexed with a lipid to form a lipid construct of the invention. The
CC      lipid constructs of the invention also contain an aminomannose
CC      derivatised cholesterol, such as derivatised
CC      dioleoylphosphatidylethanolamine (DOPE). The aminomannose used is
CC      preferably 6-(cholest-5-en-3beta-yloxy)hexyl 6-amino-6-deoxy-1-thiol-
CC      alpha-D-mannopyranoside. The lipid constructs are used to target a
CC      therapeutic or imaging agent to vascular smooth muscle. By including
CC      the derivatised cholesterol in the lipid component of the liposomes, the
CC      uptake of the liposome by smooth muscle cells is greatly increased.
CC      Administration of two antisense oligonucleotides (such as this sequence
CC      and AAT51718) that block the cell-cycle regulatory genes for PCNA and
CC      cdc2 has previously been shown to inhibit neointima hyperplasia
CC      following angioplasty injury. The liposomes of the invention can be used
CC      for the delivery of an anti-restenosis oligonucleotide (that prevents
CC      neointima formation) during percutaneous transluminal coronary
CC      angioplasty (PTCA).
XX
SQ      Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match      100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 gatcaggcgtgcctcaaa 18
Db      1 gatcaggcgtgcctcaaa 18
|||||
RESULT 10
AAT51718
ID      AAT51718 standard; DNA; 18 BP.
XX
AC      AAT51718;
XX
XX      09-APR-1997 (first entry)
DT
DE
DE      Oligonucleotide 2342.
XX
KW      Antisense oligonucleotide; rat; cdc gene; lipid complex; restenosis;
KW      aminomannose derivatised cholesterol; vascular smooth muscle; liposome;
KW      cell-cycle regulatory gene; proliferating cell nuclear antigen; PTCA;
KW      inhibitor; neointima hyperplasia; angioplasty injury; PCNA;
KW      percutaneous transluminal coronary angioplasty; ss.
XX
OS      Synthetic.
XX
PN      WO9624333-A1.
XX
PD      15-AUG-1996.
XX
PF      09-FEB-1996; 96WO-US01807.
XX
PR      10-FEB-1995; 95US-0386579.
XX
PA      (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI      Male-Brunne R;
XX
DR      WPI; 1996-384195/38.
XX
PT      Vascular targeting of therapeutic or imaging agents - using
PT      liposome(s) contg. amino:mannose-derivatised cholesterol
XX
PS      Example 2; Page 17; 45pp; English.
XX
CC      This sequence represents an antisense oligonucleotide that targets the
CC      rat proliferating cell nuclear antigen (PCNA) gene. This sequence is
CC      complexed with a lipid to form a lipid construct of the invention. The
CC      lipid constructs of the invention also contain an aminomannose
CC      derivatised cholesterol, such as derivatised
CC      dioleoylphosphatidylethanolamine (DOPE). The aminomannose used is
CC      preferably 6-(cholest-5-en-3beta-yloxy)hexyl 6-amino-6-deoxy-1-thiol-
CC      alpha-D-mannopyranoside. The lipid constructs are used to target a
CC      therapeutic or imaging agent to vascular smooth muscle. By including
CC      the derivatised cholesterol in the lipid component of the liposomes, the
CC      uptake of the liposome by smooth muscle cells is greatly increased.
CC      Administration of two antisense oligonucleotides (such as this sequence
CC      and AAT51718) that block the cell-cycle regulatory genes for PCNA and
CC      cdc2 has previously been shown to inhibit neointima hyperplasia
CC      following angioplasty injury. The liposomes of the invention can be used
CC      for the delivery of an anti-restenosis oligonucleotide (that prevents
CC      neointima formation) during percutaneous transluminal coronary
CC      angioplasty (PTCA).
XX
SQ      Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match      100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 gatcaggcgtgcctcaaa 18
Db      1 gatcaggcgtgcctcaaa 18
|||||
RESULT 11
AAT39739
ID      AAT39739 standard; DNA; 18 BP.
XX
AC      AAT39739;
XX
XX      15-APR-1997 (first entry)
DT
DE
DE      Rat PCNA gene antisense oligonucleotide.
XX
KW      Inhibition; cancer cell; cytoplasm; vascular smooth muscle cell; nuclei;
KW      aminomannose-derivatised cholesterol component; Amch; VSMC; ss.
XX
OS      Synthetic.
XX
PN      WO9624334-A1.
XX
PD      15-AUG-1996.
XX
PF      08-FEB-1996; 96WO-US01960.
XX
PR      10-FEB-1995; 95US-0386577.
XX
PA      (NEXS-) NEXSTAR PHARM INC.
XX
PI      Male-Brunne R, Proffitt R;
XX
DR      WPI; 1996-384196/38.
XX
PT      Novel lipid construct contg. an amino:mannose-derivatised
PT      cholesterol - useful for delivery of therapeutic or imaging agent to
PT      cell cytoplasm, esp. for anti-sense oligo:nucleotide(s) used to
PT      inhibit growth of e.g. cancers
XX
PS      Claim 21; Page 40; 49pp; English.
XX
CC      The sequences given in AAT39738-39 represent oligonucleotides which
CC      may be used in the method of the invention to inhibit the growth of
CC      vascular smooth muscle cells. The oligonucleotides are administered
CC      to the cytoplasm of a cell by administration of a lipid construct that
CC      includes an aminomannose-derivatised cholesterol component. The
CC      aminomannose-derivatised component is pref. 6-(cholest-5-en-3beta-
CC      yloxy)hexyl-6-amino-6-deoxy-1-thio-alpha-D-mannopyranoside (Amch).
CC      The use of a derivatised cholesterol component provides targeting
CC      to vascular smooth muscle cells without the use of viral material
CC      and the lipid construct allows more efficient delivery of
CC      oligonucleotides to the cytoplasm and nuclei than known constructs.
CC      The oligonucleotides can be used to inhibit the growth of cancer cells.
XX
SQ      Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match      100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 gatcaggcgtgcctcaaa 18
Db      1 gatcaggcgtgcctcaaa 18
|||||
RESULT 12
AAT39739
ID      AAT39739 standard; DNA; 18 BP.
XX
AC      AAT39739;
XX
XX      27-JUL-2000 (first entry)
DT
DE
DE      PCNA phosphorothioate antisense oligonucleotide SEQ ID NO:7.
XX
KW      Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW      PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW      recurrent stenosis; cardiovascular injury; ss.

```

```

XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT modified_base 1..18
XX FT /*tag= a
XX FT /note= "phosphorothioate linkages"
XX
XX CA2228977-A1.
XX PN
XX XX
XX PD 07-MAY-1999.
XX PF
XX PE 03-FEB-1998; 98CA-2228977.
XX PR
XX XX 07-NOV-1997; 97CA-2215360.
XX PA (EDEL/) EDELMAN E R.
XX PA (ROSE/) ROSENBERG R D.
XX PA (SIRO/) SIROIS M G.
XX PA (SIRO/) SIROIS M.
XX XX
XX PI Edelman ER, Rosenberg RD, Siros MG, Simons M;
XX XX WPI; 2000-283933/25.
XX XX
XX XX Antisense inhibition of platelet derived growth factor beta-receptor
XX PT subunit expression for the prevention of restenosis -
XX XX
XX PS Claim 27; Page 27; 43pp; English.
XX XX
XX CC A method has been developed for preventing restenosis following vascular
XX CC injury by antisense inhibition of platelet derived growth factor
XX CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
XX CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
XX CC canal), especially of a valve in the heart, after surgical correction of
XX CC the primary condition) following cardiovascular injury. The present
XX CC sequence represents a phosphorothioate antisense oligonucleotide for
XX CC PCNA.
XX XX
XX XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 18; DB 21; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 gatcaggcgtgcctcaaa 18
XX |||||||
XX Db 1 gatcaggcgtgcctcaaa 18
XX
XX
XX RESULT 12
XX AAF60953
XX ID AAF60953 standard; DNA; 18 BP.
XX XX
XX AC AAF60953;
XX XX
XX XX 15-MAY-2001 (first entry)
XX XX
XX XX Anti-PCNA oligonucleotide SEQ ID 62.
XX XX
XX XX Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
XX KW antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense;
XX KW tumor therapy; drug; ss.
XX XX
XX OS Unidentified.
XX XX
XX PN DE19935302-A1.
XX XX
XX PD 08-FEB-2001.
XX XX
XX PF 28-JUL-1999; 99DE-1035302.
XX XX

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PR XX 28-JUL-1999; 99DE-1035302.
XX PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
XX XX WPI; 2001-203679/21.
XX XX
XX PT New substituted aryl conjugates of parent molecules, especially
XX PT oligonucleotides, having improved transmembrane and intracellular
XX PT transport properties, useful as medicaments or diagnostic agents -
XX XX
XX PS Disclosure; Page 8; 28pp; German.
XX XX
XX CC This invention describes a novel conjugate (I) which consists of (A) a
XX CC molecule to be transported and (B) at least one aryl residue of formula
XX CC -Ar-(X-C(Y)-R1)n (II). Ar = group containing at least one aromatic
XX CC ring; X = O or N (sic); Y = O, S or NH-R2 (sic); R1 = optionally
XX CC substituted 1-23C alkyl (optionally containing double and/or triple
XX CC bonds); R2 = optionally substituted 1-18C alkyl (optionally containing
XX CC double and/or triple bonds); n = integer of 1 or more. (A) is bonded to
XX CC (B) directly or via a chemical group, provided that the chemical group is
XX CC other than CH2-S if the bond is via a phosphodiester linkage of (A). The
XX CC invention also describes (i) the preparation of a conjugate (I') of (A')
XX CC a molecule to be transported and (B') at least one aryl residue (not
XX CC restricted to (II)), by preparing (A') containing a reactive function at
XX CC the position at which (B') is to be bonded, preparing (B') and reacting
XX CC (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded
XX CC via a chemical group) for transporting (A) across biological membranes.
XX CC The products of the invention have cytostatic, virucide, vasotropic,
XX CC dermatological, antipsoriatic and antiasthmatic activity and can be used
XX CC for gene therapy. Conjugation of (A) with (B) is useful for transporting
XX CC (A) across biological membranes or into eukaryotic or prokaryotic cells
XX CC (specifically bacterial, yeast or mammalian cells, including human cells,
XX CC particularly tumor cells). Medicaments, diagnostic agents and test kits
XX CC containing (I) are also claimed. Typically (I) are antisense
XX CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
XX CC treating viral infections or diseases associated with integrins or
XX CC cell-cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma);
XX CC or labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
XX CC hybridization. Conjugation with (B) markedly improves the cellular uptake
XX CC of (A), e.g. in tumor cells. (B) include fluorescently labeled, allowing
XX CC in which case the conjugates (I) are fluorescently labeled, allowing
XX CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
XX CC is superior to that obtained using other conjugated groups related to
XX CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
XX CC the scope of (B)) have superior uptake to corresponding fluorescein
XX CC conjugates.
XX XX
XX XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 18; DB 22; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 gatcaggcgtgcctcaaa 18
XX |||||||
XX Db 1 gatcaggcgtgcctcaaa 18
XX
XX
XX RESULT 13
XX AAH49236
XX ID AAH49236 standard; DNA; 18 BP.
XX XX
XX AC AAH49236;
XX XX
XX XX 26-NOV-2001 (first entry)
XX XX
XX DE Anti-PCNA (proliferating cell nuclear antigen) oligonucleotide XXIX.
XX KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
XX KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;

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```
XX AAQ37751;
AC
XX
XX DT 17-DEC-2001 (updated)
XX DT 30-JUN-1993 (first entry)
XX
XX PCNA mRNA anti-sense oligonucleotide target sequence.
XX
XX Cellular division cycle; cdc; proliferating cell nuclear antigen; ss.
XX
XX Non-human.
XX
XX USN7821415-N.
XX
XX PD 01-JAN-1993.
XX
XX 14-JAN-1992; 92US-0821415.
XX
XX 14-JAN-1992; 92US-0821415.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
XX Epstein S, Speir E, Unger E;
XX
XX WPI; 1993-085860/10.
XX
XX Inhibition of re-stenosis of blood vessel - after mechanical
XX treatment, to reduce stenosis, using anti-sense oligo:nucleotide(s)
XX
XX Disclosure; Page 37; 4lpp; English.
XX
XX The sequence is that of a PCNA mRNA target sequence for antisense
XX oligonucleotides which may be used for inhibiting translation of
XX cellular division cycle (cdc) gene products. They may be used in a
XX method of inhibiting restenosis of a mammalian blood vessel after
XX mechanical treatment to reduce a stenosis, e.g. coronary balloon
XX angioplasty. The sequence spans the AUG translation initiation codon.
XX (Note: Revised entry submitted to correct the patent number format of
XX US Government-owned NTIS applications to prevent clashes with ongoing US
XX granted patent numbers. For further information please visit the Derwent
XX web site at www.derwent.com/dwpl/updates/ntis\_us.html.)
XX
XX Sequence 27 BP; 5 A; 9 C; 7 G; 6 U; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcagcgctgcctcaaa 18
   |||||||
Db 27 GATCAGCGCTGCCTCAAA 10

Search completed: October 12, 2002, 17:08:05
Job time: 9750 sec
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:38 ; Search time 191.26 Seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-7

Perfect score: 18
Sequence: 1 gatcaggcggtgcctcaaa 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTus_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	1	US-08-369-282-5
2	18	100.0	18	1	US-08-241-372-22
3	18	100.0	18	1	US-08-241-372-24
4	18	100.0	18	1	US-08-386-579-2
5	18	100.0	18	1	US-08-110-294A-17
6	18	100.0	18	1	US-08-110-294A-19
7	18	100.0	18	1	US-08-110-294A-38
8	18	100.0	18	1	US-08-110-294A-39
9	18	100.0	18	2	US-08-389-926-17
10	18	100.0	18	2	US-08-389-926-19
11	18	100.0	18	2	US-08-389-926-38
12	18	100.0	18	2	US-08-389-926-39
13	18	100.0	18	3	US-08-578-686C-28
14	18	100.0	18	3	US-08-094-405-23
15	18	100.0	18	3	US-08-144-112-28
16	18	100.0	18	4	US-08-337-120A-23
17	18	100.0	18	5	PCT-US92-00626-5
18	18	100.0	18	5	PCT-US95-05420-22
19	18	100.0	18	5	PCT-US95-05420-24
20	18	100.0	18	5	PCT-US96-01807-2
21	18	100.0	27	1	US-08-187-785-12
22	15	83.3	30	1	US-08-241-372-21
23	15	83.3	30	5	PCT-US95-05420-21
24	13.4	74.4	30	1	US-08-110-294A-15
25	13.4	74.4	30	2	US-08-389-926-15
26	13.2	73.3	18	2	US-08-389-926-53
27	13.2	73.3	34	3	US-08-950-860-10

c 28	13.2	73.3	39	1	US-08-465-293A-7	Sequence 7, Appli
c 29	13.2	73.3	39	2	US-08-463-387A-7	Sequence 7, Appli
c 30	13.2	73.3	39	3	US-09-102-977-8	Sequence 8, Appli
c 31	13.2	73.3	39	4	US-09-034-088A-22	Sequence 22, Appli
c 32	12.8	71.1	27	2	US-08-692-787-57	Sequence 57, Appli
c 33	12.8	71.1	27	4	US-09-097-199-57	Sequence 92, Appli
c 34	12.8	71.1	46	1	US-08-271-880A-92	Sequence 92, Appli
c 35	12.8	71.1	46	1	US-08-271-880A-115	Sequence 115, App
c 36	12.8	71.1	46	2	US-08-910-408-92	Sequence 92, Appli
c 37	12.8	71.1	46	2	US-08-910-408-115	Sequence 115, App
c 38	12.8	71.1	46	3	US-09-249-215-92	Sequence 92, Appli
c 39	12.8	71.1	46	3	US-09-249-215-115	Sequence 115, App
c 40	12.4	68.9	38	3	US-09-120-386-3	Sequence 3, Appli
c 41	12.4	68.9	38	4	US-09-120-501-3	Sequence 3, Appli
c 42	12.4	68.9	39	3	US-09-120-386-4	Sequence 4, Appli
c 43	12.4	68.9	39	4	US-09-120-501-4	Sequence 4, Appli
c 44	12.2	67.8	18	1	US-08-187-785-6	Sequence 6, Appli
c 45	12.2	67.8	20	1	US-08-116-389-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-08-369-282-5
; Sequence 5, Application US/08369282
; Patent No. 5593974
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, ROBERT D
; APPLICANT: SIMONS, MICHAEL
; APPLICANT: EDELMAN, ELAZER
; APPLICANT: LANGER, ROBERT S
; APPLICANT: DEKEYSER, JEAN-LUC
; TITLE OF INVENTION: LOCALIZED OLIGONUCLEOTIDE THERAPY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,282
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/855,416
; FILING DATE:
; APPLICATION NUMBER: US 792,146
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 723,454
; FILING DATE: 28-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MIT5583CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna

; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /standard_name= "ANTISENSE PCNA"
; OTHER INFORMATION: /note= "ANTISENSE SEQUENCE TO PCNA"
US-08-369-282-5

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGGCGTGCCTCAAA 18

RESULT 2
US-08-241-372-22
; Sequence 22, Application US/08241372
; Patent No. 5631237
; GENERAL INFORMATION:
; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: METHOD FOR IN VIVO DELIVERY OF
; TITLE OF INVENTION: THERAPEUTIC AGENTS VIA LIPOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,372
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-59079-1/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-241-372-22

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGGCGTGCCTCAAA 18

RESULT 3
US-08-241-372-24/c

; Sequence 24, Application US/08241372
; Patent No. 5631237
; GENERAL INFORMATION:
; APPLICANT: Dzaou, Victor J
; APPLICANT: Kaneda, Ysasufumi
; TITLE OF INVENTION: METHOD FOR IN VIVO DELIVERY OF
; TITLE OF INVENTION: THERAPEUTIC AGENTS VIA LIPOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,372
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-59079-1/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-241-372-24

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 4
US-08-386-579-2
; Sequence 2, Application US/08386579
; Patent No. 5660855
; GENERAL INFORMATION:
; APPLICANT: M le-Brune, Roxanne
; TITLE OF INVENTION: LIPID CONSTRUCTS FOR TARGETING TO
; TITLE OF INVENTION: VASCULAR SMOOTH MUSCLE TISSUE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vestar, Inc.
; STREET: 650 Cliffside Drive
; CITY: San Dimas
; STATE: California
; COUNTRY: USA
; ZIP: 91773
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/386,579
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cochran, Adam
; REGISTRATION NUMBER: 29,373
; REFERENCE/DOCKET NUMBER: D89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (909)-394-4132
; TELEFAX:
; TYPE:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-386-579-2

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
DB 1 GATCAGCGTGCCTCAAA 18

RESULT 5

US-08-110-294A-17
; Sequence 17, Application US/08110294A
; Patent No. 5821234
; GENERAL INFORMATION:

; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/110,294A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-110-294A-17

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
DB 1 GATCAGCGTGCCTCAAA 18

RESULT 6

US-08-110-294A-19/c
; Sequence 19, Application US/08110294A
; Patent No. 5821234
; GENERAL INFORMATION:

; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/110,294A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234

; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-110-294A-19

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
DB 18 GATCAGCGTGCCTCAAA 1

```
RESULT 7
US-08-110-294A-38/c
; Sequence 38, Application US/08110294A
; Patent No. 5821234
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-110-294A-38

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcggtgcctcaaa 18
   |||||
Db 18 GATCAGCGGTGCTCAAA 1

RESULT 8
US-08-110-294A-39
; Sequence 39, Application US/08110294A
; Patent No. 5821234
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,926
; FILING DATE: 16 FEB 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-110-294A-39

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcggtgcctcaaa 18
   |||||
Db 1 GATCAGCGGTGCTCAAA 18

RESULT 9
US-08-389-926-17
; Sequence 17, Application US/08389926
; Patent No. 5869462
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,926
; FILING DATE: 16 FEB 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
```

ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,510-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-389-926-17

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 18

RESULT 10
US-08-389-926-19/c
; Sequence 19, Application US/08389926
; Patent No. 5869462
; GENERAL INFORMATION:
; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,926
; FILING DATE: 16 FEB 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-389-926-19

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 1

RESULT 11
US-08-389-926-38/c
; Sequence 38, Application US/08389926
; Patent No. 5869462
; GENERAL INFORMATION:
; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,926
; FILING DATE: 16 FEB 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-389-926-38

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 1

RESULT 12
US-08-389-926-39
; Sequence 39, Application US/08389926
; Patent No. 5869462

;; GENERAL INFORMATION:
;; APPLICANT: Dzau, Victor J
;; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
;; TITLE OF INVENTION: Smooth Muscle Cell
;; NUMBER OF SEQUENCES: 53
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Dr.
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/389,926
;; FILING DATE: 16 FEB 1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/063,980
;; FILING DATE: 19-MAY-1993
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/944,882
;; FILING DATE: 10-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDonnell, John J
;; REGISTRATION NUMBER: 26,949
;; REFERENCE/DOCKET NUMBER: 93,510-D
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; INFORMATION FOR SEQ ID NO: 39:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; US-08-389-926-39

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGTGCCTCAAA 18

RESULT 13
US-08-578-686C-28
; Sequence 28, Application US/08578686C
; Patent No. 6028182
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; TITLE OF INVENTION: Methylphosphonic Acid Ester, Process For
; TITLE OF INVENTION: Preparing The Same And Its Use
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I. Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/578,686C
;; FILING DATE: January 2, 1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Johnson, Lori-Ann
;; REGISTRATION NUMBER: 34,498
;; REFERENCE/DOCKET NUMBER: 2481.1481-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-578-686C-28

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGTGCCTCAAA 18

RESULT 14
US-09-094-405-23
; Sequence 23, Application US/09094405
; Patent No. 6066720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified oligonucleotides, their preparation
; TITLE OF INVENTION: and use
; NUMBER OF SEQUENCES: 30
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,405
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,196
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..18
; OTHER INFORMATION: /note= "PCNA (proliferating cell
; OTHER INFORMATION: nuclear antigen)"
; US-09-094-405-23

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctgctcaaa 18
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Db 1 GATCAGCGCTGCTCAAA 18

RESULT 15
US-09-144-112-28
; Sequence 28, Application US/09144112
; Patent No. 6150510
; GENERAL INFORMATION:
; APPLICANT: SEELA, Frank
; APPLICANT: THOMAS, Horst
; TITLE OF INVENTION: MODIFIED OLIGONUCLEOTIDES, THEIR PREPARATION AND THEIR
; TITLE OF INVENTION: USE
; FILE REFERENCE: 026083/0181
; CURRENT APPLICATION NUMBER: US/09/144,112
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: DE P 44 38 918.3
; PRIOR FILING DATE: 1994-11-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antisense
; OTHER INFORMATION: Oligonucleotide
US-09-144-112-28

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctgctcaaa 18
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Db 1 GATCAGCGCTGCTCAAA 18

Search completed: October 12, 2002, 16:54:38
Job time: 8993 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:32 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-7

Perfect score: 18

Sequence: 1 gatcaggcgtgcctcaaa 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 58: /cgn2_6/ptodata/2/pna/US6019_COMB.seq.*
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- 61: /cgn2_6/ptodata/2/pna/US6022_COMB.seq.*
- 62: /cgn2_6/ptodata/2/pna/US6023_COMB.seq.*
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- 64: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
- 65: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
- 66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
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- 70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
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- 72: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
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- 74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	3	US-07-944-882-22	Sequence 22, Appl
	18	100.0	18	3	US-07-944-882-24	Sequence 24, Appl
	c	2	18	100.0	18	3
c	4	18	100.0	18	3	Sequence 22, Appl
	5	18	100.0	18	5	Sequence 17, Appl
c	6	18	100.0	18	5	Sequence 19, Appl
	7	18	100.0	18	5	Sequence 38, Appl
c	8	18	100.0	18	5	Sequence 39, Appl
	9	18	100.0	18	6	Sequence 22, Appl
c	10	18	100.0	18	6	Sequence 24, Appl
	11	18	100.0	18	7	Sequence 22, Appl
c	12	18	100.0	18	8	Sequence 28, Appl
	13	18	100.0	18	8	Sequence 2, Appl
c	14	18	100.0	18	8	Sequence 2, Appl
	15	18	100.0	18	8	Sequence 2, Appl
c	16	18	100.0	18	10	Sequence 17, Appl
	17	18	100.0	18	10	Sequence 19, Appl
	18	18	100.0	18	13	Sequence 23, Appl
c	19	18	100.0	18	16	Sequence 7, Appl
	20	18	100.0	18	24	Sequence 62, Appl
c	21	18	100.0	18	25	Sequence 28, Appl
	22	18	100.0	18	30	Sequence 28, Appl
c	23	18	100.0	18	32	Sequence 51, Appl
	24	18	100.0	18	32	Sequence 51, Appl
c	25	15	83.3	30	3	Sequence 19, Appl
	26	15	83.3	30	3	Sequence 19, Appl
c	27	15	83.3	30	6	Sequence 21, Appl
	28	13.8	76.7	25	74	Sequence 17512,
c	29	13.8	76.7	25	74	Sequence 169230,
	30	13.4	74.4	25	74	Sequence 207077,
c	31	13.4	74.4	30	5	Sequence 15, Appl
	32	13.4	74.4	30	5	Sequence 15, Appl

c 32 13.4 74.4 30 10 US-08-632-758-15 Sequence 15, Appl
c 33 13.4 74.4 37 29 US-09-746-375-21 Sequence 21, Appl
c 34 13.2 73.3 33 10 US-08-617-833-111 Sequence 111, Appl
c 35 13.2 73.3 33 10 US-08-617-833H-111 Sequence 111, Appl
c 36 13.2 73.3 34 13 US-08-950-860-10 Sequence 10, Appl
c 37 13.2 73.3 34 13 US-08-950-860B-10 Sequence 10, Appl
c 38 13.2 73.3 34 19 US-09-517-177-10 Sequence 10, Appl
c 39 13.2 73.3 39 4 US-08-064-385C-7 Sequence 7, Appl
c 40 13.2 73.3 39 4 US-08-064-385D-8 Sequence 8, Appl
c 41 13.2 73.3 39 8 US-08-465-292-7 Sequence 7, Appl
c 42 13.2 73.3 39 12 US-08-899-134-7 Sequence 7, Appl
c 43 13.2 73.3 39 30 US-09-781-811-22 Sequence 22, Appl
c 44 12.8 71.1 24 35 US-09-940-185-2835 Sequence 2835, Ap
c 45 12.8 71.1 25 35 US-09-954-427-84417 Sequence 84417, A

ALIGNMENTS

RESULT 1
US-07-944-882-22
; Sequence 22, Application US/07944882
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J.
; APPLICANT: Pratt, Richard
; APPLICANT: Gibbons, Gary
; TITLE OF INVENTION: INHIBITION OF PROLIFERATION OF VASCULAR
; TITLE OF INVENTION: SMOOTH MUSCLE CELL
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/944,882
; FILING DATE: 19920910
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-56837/BIR;STAN-137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 22:

LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-944-882-22

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
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Db 1 GATCAGCGTGCCTCAAA 18

RESULT 2
US-07-944-882-24/c

; Sequence 24, Application US/07944882
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J.
; APPLICANT: Pratt, Richard
; APPLICANT: Gibbons, Gary
; TITLE OF INVENTION: INHIBITION OF PROLIFERATION OF VASCULAR
; TITLE OF INVENTION: SMOOTH MUSCLE CELL
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/944,882
; FILING DATE: 19920910
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-56837/BIR;STAN-137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 24:

LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-944-882-24

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
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Db 18 GATCAGCGTGCCTCAAA 1

RESULT 3
US-07-995-022-20
; Sequence 20, Application US/07995022
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J.
; TITLE OF INVENTION: Methods for in vivo delivery of
; TITLE OF INVENTION: therapeutic agents via HVJ-liposomes to cells of the
; TITLE OF INVENTION: vasculature
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: Ten South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/995,022

; FILING DATE: 19921222
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,752
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; STRAIN: single
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /note= "ANTISENSE CYCLIN A +4 -
; OTHER INFORMATION: +21"
US-07-995-022-20

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
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Db 1 GATCAGGCGTGCCTCAAA 18

RESULT 4
US-07-995-022-22/c
; Sequence 22, Application US/07995022
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Methods for in vivo delivery of
; TITLE OF INVENTION: therapeutic agents via HVJ-liposomes to cells of the
; TITLE OF INVENTION: vasculature
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: Ten South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07995,022
; FILING DATE: 19921222
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,752
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs

; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /note= "CONTROL SENSE CYCLIN A +4 -
; OTHER INFORMATION: +21"
US-07-995-022-22

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
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Db 1 GATCAGGCGTGCCTCAAA 1

RESULT 5
US-08-110-294-17
; Sequence 17, Application US/08110294
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/110,294
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-110-294-17

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18

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Db 1 GATCAGGCGTGCCTCAAA 18
|||||
RESULT 6
US-08-110-294-19/c
; Sequence 19, Application US/08110294
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-110-294-38

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcggtgcctcaaa 18
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 8
US-08-110-294-39
; Sequence 39, Application US/08110294
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-110-294-19

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcggtgcctcaaa 18
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 7
US-08-110-294-38/c
; Sequence 38, Application US/08110294
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-110-294-19
```

ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,510-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-110-294-39

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||

Db 1 GATCAGCGTGCCTCAAA 18

RESULT 9
US-08-240-106-22
Sequence 22, Application US/08240106
GENERAL INFORMATION:
APPLICANT: Dzau, Victor J
TITLE OF INVENTION: METHOD FOR IN VIVO DELIVERY OF
TITLE OF INVENTION: THERAPEUTIC AGENTS VIA LIPOSOMES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,106
FILING DATE: 09-MAY-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-59079-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-240-106-22

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||

Db 1 GATCAGCGTGCCTCAAA 18

RESULT 10
US-08-240-106-24/c
Sequence 24, Application US/08240106
GENERAL INFORMATION:
APPLICANT: Dzau, Victor J
TITLE OF INVENTION: METHOD FOR IN VIVO DELIVERY OF
TITLE OF INVENTION: THERAPEUTIC AGENTS VIA LIPOSOMES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,106
FILING DATE: 09-MAY-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-59079-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-240-106-24

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||

Db 18 GATCAGCGTGCCTCAAA 1

RESULT 11
US-08-386-577-2
Sequence 2, Application US/08386577
GENERAL INFORMATION:
APPLICANT: M le-Brune, Roxanne
TITLE OF INVENTION: LIPID CONSTRUCTS FOR CYTOPLASMIC DELIVERY
TITLE OF INVENTION: OF AGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vestar, Inc.
STREET: 650 Cliffside Drive
CITY: San Dimas
STATE: California
COUNTRY: USA
ZIP: 91773

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386.577
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cochran, Adam
; REGISTRATION NUMBER: 29,373
; REFERENCE/DOCKET NUMBER: D90
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (909)-394-4132
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-386-577-2
```

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Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 gatcaggcgctgctcaaa 18
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DB 1 GATCAGCGCTGCCTCAAA 18
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RESULT 12
US-08-402-838-28
; Sequence 28, Application US/08402838
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; TITLE OF INVENTION: Polymide-Oligonucleotide Derivatives,
; TITLE OF INVENTION: Their Preparation And Use
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,838
; FILING DATE: 13-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Warnement, Thalia V.
; REGISTRATION NUMBER: 39,064
; REFERENCE/DOCKET NUMBER: 02481.1437-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
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```
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-402-838-28

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctgctcaaa 18
|||||
DB 1 GATCAGCGCTGCCTCAAA 18

RESULT 13
US-08-463-012-2
; Sequence 2, Application US/08463012
; GENERAL INFORMATION:
; APPLICANT: Profit, Richard T.
; TITLE OF INVENTION: LIPID CONSTRUCTS FOR CYTOLASMIC DELIVERY
; TITLE OF INVENTION: OF AGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vestar, Inc.
; STREET: 650 Cliffside Drive
; CITY: San Dimas
; STATE: California
; COUNTRY: USA
; ZIP: 91773
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 .
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,012
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cochran, Adam
; REGISTRATION NUMBER: 29,373
; REFERENCE/DOCKET NUMBER: D90B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (909)-394-4132
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-463-012-2
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Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctgctcaaa 18
|||||
DB 1 GATCAGCGCTGCCTCAAA 18
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```
RESULT 14
US-08-463-013-2
; Sequence 2, Application US/08463013
```


GENERAL INFORMATION:
APPLICANT: M le-Brune, Roxanne
TITLE OF INVENTION: LIPID CONSTRUCTS FOR CYTOPLASMIC DELIVERY
TITLE OF INVENTION: OF AGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vestar, Inc.
STREET: 650 Cliffside Drive
CITY: San Dimas
STATE: California
COUNTRY: USA
ZIP: 91773
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,013
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cochran, Adam
REGISTRATION NUMBER: 29,373
REFERENCE/DOCKET NUMBER: D90A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (909)-394-4132
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-463-013-2

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGGCGTGCTCAAA 18

RESULT 15
US-08-463-014-2
Sequence 2, Application US/08463014
GENERAL INFORMATION:
APPLICANT: M le-Brune, Roxanne
TITLE OF INVENTION: LIPID CONSTRUCTS FOR CYTOPLASMIC DELIVERY
TITLE OF INVENTION: OF AGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vestar, Inc.
STREET: 650 Cliffside Drive
CITY: San Dimas
STATE: California
COUNTRY: USA
ZIP: 91773
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,014
FILING DATE: 10-FEB-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cochran, Adam
REGISTRATION NUMBER: 29,373
REFERENCE/DOCKET NUMBER: D90C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (909)-394-4132
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-463-014-2

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGGCGTGCTCAAA 18

Search completed: October 12, 2002, 20:42:33
Job time: 16403 sec

2002